



the complementarity determining regions (CDRs) of murine anti-IL-8 antibody 6G4.2.5 (see W69309) light chain within a human 6-subgroup I light chain template. Humanised anti-IL-8 monoclonal antibodies (MABs) and variants are described for use in diagnostic applications and in the treatment of inflammatory disorders. The invention provides conjugates of an antibody fragment and a non-proteinaceous polymer, such as PEG, that have improved half-life, mean residence time, and/or clearance rate compared to non-derivatised parental antibody fragment. Also claimed are a polypeptide that is an anti-IL-8 MAB or antibody fragment comprising a light chain amino acid sequence comprising the light chain CDRs of 6G4.2.5/ILN35A, a nucleic acid encoding such a polypeptide, and a method of producing the polypeptide in host cells. The conjugates can be used for immune therapy of inflammatory bowel disorders, e.g. psoriasis, responses associated with inflammatory bowel disease (such as Crohn's disease and ulcerative colitis), ischemic reperfusion, adult respiratory distress syndrome, dermatitis, meningitis, encephalitis, uveitis, autoimmune diseases such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis, diseases involving leukocyte diapedesis, central nervous system inflammatory disorder, multiple organ injury syndrome secondary to septicemia or trauma, alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex mediated diseases, inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and cystic fibrosis. They can also be used in diagnostic applications

Query Match 100.0%; Score 1679; DB 1; Length 242;  
Best Local Similarity 100.0%; Pred. No. 4,36e-117;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKNNIAFLASMFVSIATNAYADIQTQSPSSLSASVGDVITTCRSSQLVHGIGATY 60  
QY 1 MKNNIAFLASMFVSIATNAYADIQTQSPSSLSASVGDVITTCRSSQLVHGIGATY 60  
Db 61 LHWYQKPKAPKLLIYKVNRFSGVPSRSGSGSDFTLTIISSLOPEDFATYCSQST 120  
QY 61 LHWYQKPKAPKLLIYKVNRFSGVPSRSGSGSDFTLTIISSLOPEDFATYCSQST 120  
Db 121 HVPLTFGGTKVEIKRTVAAPSVFIPTPPSDEQLKSGTASVCLLNFPYPRKQVQKVDN 180  
QY 121 HVPLTFGGTKVEIKRTVAAPSVFIPTPPSDEQLKSGTASVCLLNFPYPRKQVQKVDN 180  
Db 181 ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240  
QY 181 ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240  
241 EC 242  
241 EC 242

RESULT 2  
ID W69313 standard; Protein: 242 AA.  
AC W69313;  
DE 15-FEB-1999 (first entry)  
DE Anti-IL-8 humanised antibody 6G4V11N35A.F(ab')2.  
KW Humanised antibody; chimeric antibody; monoclonal antibody; mouse;  
KW human; Fab; interleukin-8, inflammation, immunotherapy, psoriasis;  
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW ischaemic reperfusion; adult respiratory distress syndrome;  
KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;  
KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;  
KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;  
KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;  
KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;  
KW therapy: p6G4V11N35A.F(ab')2.  
OS Chimeric - Mus sp.  
OS Location/Qualifiers  
FH Key 439..1167  
FT CDS /\*tag= a  
FT W6937200\*2.

27-AUG-1998 PD  
20-FEB-1998 PF  
22-JAN-1998 PR  
21-FEB-1997 PR  
PA (GETH) GENENTECH INC.  
PI Hsui V, Koumenis I, Leong SR, Presta LR, Shahrokh Z.  
PI Zapata GA;  
DR WPI: 98-467563/40.  
DR N-PSDB: V44953.  
DR New conjugates of antibody fragments - having covalently attached non-proteinaceous polymer molecules, particularly polyethylene glycol, for improving the residence time in the circulation.  
PS Example K; Fig 4B-D: 328pp; English.  
CC This is the amino acid sequence of a polypeptide encoded by plasmid p6G4V11N35A.F(ab')2 (see V44953), comprising a murine-human chimeric Fab containing complementarity determining regions of murine anti-interleukin-8 (IL-8) monoclonal antibody (MAB) 6G5.2.5 (see W69309-10) in a human template. Humanised anti-IL-8 MABs (see W69301-04) are described for use in diagnostic applications and in the treatment of inflammatory disorders. The invention provides conjugates of an antibody fragment and a polymer, such as PEG, that have improved half-life, mean residence time, and/or clearance rate. The conjugates can be used for immune therapy of e.g. psoriasis, Crohn's disease and ulcerative colitis, ischemic reperfusion, adult respiratory distress syndrome, dermatitis, meningitis, encephalitis, uveitis, autoimmune diseases such as rheumatoid arthritis, Sjorgen's syndrome, vasculitis, diseases involving leukocyte diapedesis, central nervous system inflammatory disorder, multiple organ injury syndrome secondary to septicemia or trauma, alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex mediated diseases, inflammations of the lung, including pleurisy, alveolitis, vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and cystic fibrosis.  
SQ Sequence 242 AA;

Query Match 100.0%; Score 1679; DB 1; Length 242;  
Best Local Similarity 100.0%; Pred. No. 4,36e-117;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKNNIAFLASMFVSIATNAYADIQTQSPSSLSASVGDVITTCRSSQLVHGIGATY 60  
QY 1 MKNNIAFLASMFVSIATNAYADIQTQSPSSLSASVGDVITTCRSSQLVHGIGATY 60  
Db 61 LHWYQKPKAPKLLIYKVNRFSGVPSRSGSGSDFTLTIISSLOPEDFATYCSQST 120  
QY 61 LHWYQKPKAPKLLIYKVNRFSGVPSRSGSGSDFTLTIISSLOPEDFATYCSQST 120  
Db 121 HVPLTFGGTKVEIKRTVAAPSVFIPTPPSDEQLKSGTASVCLLNFPYPRKQVQKVDN 180  
QY 121 HVPLTFGGTKVEIKRTVAAPSVFIPTPPSDEQLKSGTASVCLLNFPYPRKQVQKVDN 180  
Db 181 ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240  
QY 181 ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240  
241 EC 242  
241 EC 242

RESULT 3  
ID W69302 standard; Protein: 242 AA.  
AC W69302;  
DE 15-FEB-1999 (first entry)  
DE Humanised anti-IL-8 6G4V11N35E light chain.  
KW Humanised antibody; monoclonal antibody; interleukin-8;  
KW 6G4V11N35E, inflammation, immunotherapy, therapy: psoriasis;  
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW ischaemic reperfusion; adult respiratory distress syndrome;  
KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;  
KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;  
KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;











RESULT 11  
 ID W95622 standard, Protein: 237 AA.  
 AC K25622.  
 DT 08-JUN-1999 (first entry)  
 DE p5110 expression cassette encoded rhumAb CD18 light chain.  
 KW Murine anti-CD18 antibody, heavy chain, humanized; myocardial infarction.  
 KW Burns: thermal injury; ischemic; shock; ischaemic; haemorrhagic;  
 KW hemorhagic; stroke; light chain.  
 OS Mus musculus.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Sig-Sequence 1..23  
 PN W95622-18-A1.  
 PD 17-DEC-1998.  
 PR 12-JUN-1999; US-874897  
 PA (GETH ) GENENTECH INC.  
 PI Blank GS, Narindray DS, Zapata GA.  
 DR WPI: 99-060267/05.  
 DR N-PSDB: X03840.  
 PT New method for recovering polypeptides from cell cultures - by  
 PT treating with reagent and filtering to remove reagent  
 PS Example; Fig 4: 43pp; English  
 CC A method has been developed for recovering a polypeptide comprising (a)  
 CC exposing a composition comprising a polypeptide to a reagent which binds  
 CC to or modifies the polypeptide, where the reagent is immobilized on a  
 CC solid phase; and (b) passing the composition through a filter bearing an  
 CC opposite charge to the reagent so as to remove leached reagent from the  
 CC composition. The present invention also describes a method for modifying  
 CC a precursor antibody comprising a leucine zipper by exposing the  
 CC precursor antibody to a protease immobilized on a solid support so that  
 CC the protease removes the zipper. The methods can be used to purify  
 CC proteins from cell cultures. They are especially useful for isolating  
 CC antibodies. The methods overcome the problem of reagent leakage into the  
 CC protein as is the case in prior art immobilized modification systems. By  
 CC using a opposite charge filter the reagent can be excluded from the  
 CC sample, preventing contamination. The present sequence represents the  
 CC recombinant humanised anti-CD18 antibody (rhumAb CD18) light chain,  
 CC which is used in an example from the present invention.  
 SQ Sequence 237 AA;  
 Query Match 87.0%, Score 1461, DB 1, Length 237;  
 Best Local Similarity 90.9%; Pred. No. 2 94e-100;  
 Matches 220, Conservative 5, Mismatches 12, Indels 5, Gaps 2.  
 Db 1 MKKNIAFLASMEVFSTAINAYADIQMTQSPSSLSASVGRVITICRASQD----INN-Y 55  
 QY 1 MKKNIAFLASMEVFSTAINAYADIQMTQSPSSLSASVGRVITICRASQSLVHGIGATY 60  
 Db 56 LNWYQKPKGAPKLLIYVSTLHSGVPSFSGSGSDYTLTISSLOPEDFATYYCQGN 115  
 QY 61 LHWYQKPKGAPKLLIYKVSNPFSGVPSFSGSGSDFTLTISLQPEDFATYYCQST 120  
 Db 116 TLPPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRPAKQVQKVDN 175  
 QY 121 HVPLEFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRPAKQVQKVDN 180  
 Db 176 ALQSGNSQESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 235  
 QY 181 ALQSGNSQESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240  
 Db 236 EC 237  
 QY 241 EC 242  
 RESULT 12  
 ID W95634 standard, protein: 237 AA.  
 AC W95634.  
 DT 06-APR-1999 (first entry)  
 DE Recombinant humanised anti-CD18 antibody rhumAb CD18 light chain.  
 KW Recombinant humanised anti-CD18 antibody, rhumAb CD18; leucine zipper;  
 KW murine monoclonal antibody; muMab H52; protein recovery; filtration;  
 KW chromatography.  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Reptide 1..23

FT W09856808-A1.  
 PN 17-DEC-1998.  
 PR 12-JUN-1998, U10334.  
 PA (GETH ) GENENTECH INC.  
 PI Blank GS, Narindray DS, Zapata GA.  
 DR WPI: 99-060267/05.  
 DR N-PSDB: X03840.  
 PT New method for recovering polypeptides from cell cultures - by  
 PT treating with reagent and filtering to remove reagent  
 PS Example; Fig 4: 43pp; English  
 CC A method has been developed for recovering a polypeptide comprising (a)  
 CC exposing a composition comprising a polypeptide to a reagent which binds  
 CC to or modifies the polypeptide, where the reagent is immobilized on a  
 CC solid phase; and (b) passing the composition through a filter bearing an  
 CC opposite charge to the reagent so as to remove leached reagent from the  
 CC composition. The present invention also describes a method for modifying  
 CC a precursor antibody comprising a leucine zipper by exposing the  
 CC precursor antibody to a protease immobilized on a solid support so that  
 CC the protease removes the zipper. The methods can be used to purify  
 CC proteins from cell cultures. They are especially useful for isolating  
 CC antibodies. The methods overcome the problem of reagent leakage into the  
 CC protein as is the case in prior art immobilized modification systems. By  
 CC using a opposite charge filter the reagent can be excluded from the  
 CC sample, preventing contamination. The present sequence represents the  
 CC recombinant humanised anti-CD18 antibody (rhumAb CD18) light chain,  
 CC which is used in an example from the present invention.  
 SQ Sequence 237 AA;  
 Query Match 87.0%, Score 1461, DB 1, Length 237;  
 Best Local Similarity 90.9%; Pred. No. 2 94e-100;  
 Matches 220, Conservative 5, Mismatches 12, Indels 5, Gaps 2.  
 Db 1 MKKNIAFLASMEVFSTAINAYADIQMTQSPSSLSASVGRVITICRASQD----INN-Y 55  
 QY 1 MKKNIAFLASMEVFSTAINAYADIQMTQSPSSLSASVGRVITICRASQSLVHGIGATY 60  
 Db 56 LNWYQKPKGAPKLLIYVSTLHSGVPSFSGSGSDYTLTISSLOPEDFATYYCQGN 115  
 QY 61 LHWYQKPKGAPKLLIYKVSNPFSGVPSFSGSGSDFTLTISLQPEDFATYYCQST 120  
 Db 116 TLPPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRPAKQVQKVDN 175  
 QY 121 HVPLEFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRPAKQVQKVDN 180  
 Db 176 ALQSGNSQESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 235  
 QY 181 ALQSGNSQESVTEQDSKDSSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240  
 Db 236 EC 237  
 QY 241 EC 242  
 RESULT 13  
 ID W0703 standard, Protein: 237 AA.  
 AC W0703;  
 DT 27-JAN-1999 (first entry)  
 DE Protein encoded by Fab-display antibody vector pMB4-19-1.6.  
 KW Murine; humanised antibody; VEGF-induced angiogenesis; tumour;  
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
 KW retinal disorder, age-related macular degeneration, diabetic retinopathy;  
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.  
 OS Synthetic.  
 PN W09845331-A2.  
 PD 15-OCT-1998.  
 PR 03-APR-1999; US-008469.  
 PR 06-APR-1997; US-008469.  
 PA (GETH ) GENENTECH INC.  
 PI Baca M, Chen YM, Lowman HB, Presta LG, Wells JA.  
 DR WPI: 98-568337/48.





CC the affinity molecule has affinity for the amino acid residue having the  
CC modified covalent bond, and (h) separating the phagemid particles that  
CC bind to the affinity molecule from those that do not bind. The selection  
CC method is used for identifying enzyme substrates. The present sequence  
CC represents an 4D5 Fab molecule expressed on a phagemid surface from the  
CC present invention.  
SQ Sequence 598 AA:

Query Match 85.8%, Score 1440, DB 1, Length 698:  
Residues Similarity 90.1%, Pred No 1,23e-08,  
Matches 218, Conservative 5, Mismatches 14, Indels 5, Gaps 3;  
DB 1 MKKNIAFLASMEVFSIATNAYADTQMTQSPSSLSASVGRVITTCRASQD-VN-TAVA- 57  
QY 1 MKKNIAFLASMEVFSIATNAYADTQMTQSPSSLSASVGRVITTCRASQSLVHGIGATY 60  
DB 58 --WYCKPKAPKLLIYASFLYSVPSFSSPSSTGTFILTISSLOPEDFATYYCOOHY 115  
QY 61 LHWYCKPKAPKLLIYKVSNEFSGVPSFFSGSGSGTDFILTISSLOPEDFATYYCSQT 120  
DB 116 TTPPIFGQGTIVFKPTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDN 175  
QY 121 HVPPIFGQGTIVFKPTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDN 180  
DB 176 ALQSGNSQSVTELSKSTVLSLSLLSKALYKHKVYACEVTHQGLSSPVTKSFNPG 235  
QY 181 ALQSGNSQSVTELSKSTVLSLSLLSKALYKHKVYACEVTHQGLSSPVTKSFNPG 240  
DB 236 EC 237  
QY 241 EC 242

Search completed. Thu May 18 11:45:07 2000  
Job time : 19 secs.



CC TELEX: 910/371-7168  
 CC INFORMATION FOR SEQ ID NO: 56:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 242 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC SEQUENCE 242 AA, 26430 MW, 332270 CN;  
 Query Match 99.9%, Score 1510, DB 1, Length 242;  
 Best Local Similarity 87.6%, Pred. No. 4,72e-97;  
 Matches 212: Conservative 17: Mismatches 13: Indels 0: Gaps 0:  
 Db 1 MKKNTAFLLASMFVSIATNAYADIVMTQPLSLPVSQDQASISCRSSQSLVHGIGNTY 60  
 QY 1 MKKNTAFLLASMFVSIATNAYADIVMTQPLSLPVSQDQASISCRSSQSLVHGIGATY 60  
 Db 51 LHWYLOKPGQSKLLIYKVNRFSGVDPFSGSGSGTDFTLPSVPAEDLGLYFQSGST 120  
 QY 51 LHWYLOKPGQSKLLIYKVNRFSGVDPFSGSGSGTDFTLPSVPAEDLGLYFQSGST 120  
 Db 121 HVLPTFGAGTKLEKPAVAAPTVPFPPPSSEQLKSGTASVVCLLNNFYPPKAVQWVDN 180  
 QY 121 HVLPTFGAGTKLEKPAVAAPTVPFPPPSSEQLKSGTASVVCLLNNFYPPKAVQWVDN 180  
 Db 181 ALOSGNSQESVTEQDSKSTYLSLSTLTLSKADYERHKYACEVTHQGLSSPVTAKSFNPG 240  
 QY 181 ALOSGNSQESVTEQDSKSTYLSLSTLTLSKADYERHKYACEVTHQGLSSPVTAKSFNPG 240  
 Db 241 EC 242  
 QY 241 EC 242  
 RESULT 2  
 ID US-09-234-182A-56 STANDAFC. PPT. 242 AA  
 XX xxxxxx  
 DE Sequence 56, Application US/08398612A  
 XX Sequence 56, Application US/08398612A  
 CC Patent No. 5686070  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Doershuk, Claire M.  
 CC APPLICANT: Hebert, Caroline Alice  
 CC APPLICANT: Kim, Kyung Jin  
 CC APPLICANT: Leong, Steven R.  
 CC TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for  
 CC TITLE OF INVENTION: Treatment of Inflammatory Disorders  
 CC NUMBER OF SEQUENCES: 58  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Genentech, Inc.  
 CC STREET: 460 Point San Bruno Blvd  
 CC CITY: South San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94080  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: WinPatIn (Genentech)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/398,612A  
 CC FILING DATE: 01-MAR-1995  
 CC CLASSIFICATION: 424  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: 08/398611  
 CC FILING DATE: 01-MAR-1995  
 CC APPLICATION NUMBER: 08/205864

CC FILING DATE: 03-MAR-1994  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Love, Richard B.  
 CC REGISTRATION NUMBER: 34,659  
 CC REFERENCE/DOCKET NUMBER: P0874P1  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415/223-5530  
 CC TELEFAX: 415/952-9881  
 CC TELEX: 910/371-7168  
 CC INFORMATION FOR SEQ ID NO: 56:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 242 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC SEQUENCE 242 AA, 26430 MW, 332270 CN;  
 Query Match 89.9%, Score 1510, DB 1, Length 242;  
 Best Local Similarity 87.6%, Pred. No. 4,72e-97;  
 Matches 212: Conservative 17: Mismatches 13: Indels 0: Gaps 0:  
 Db 1 MKKNTAFLLASMFVSIATNAYADIVMTQPLSLPVSQDQASISCRSSQSLVHGIGNTY 60  
 QY 1 MKKNTAFLLASMFVSIATNAYADIVMTQPLSLPVSQDQASISCRSSQSLVHGIGATY 60  
 Db 51 LHWYLOKPGQSKLLIYKVNRFSGVDPFSGSGSGTDFTLPSVPAEDLGLYFQSGST 120  
 QY 51 LHWYLOKPGQSKLLIYKVNRFSGVDPFSGSGSGTDFTLPSVPAEDLGLYFQSGST 120  
 Db 121 HVLPTFGAGTKLEKPAVAAPTVPFPPPSSEQLKSGTASVVCLLNNFYPPKAVQWVDN 180  
 QY 121 HVLPTFGAGTKLEKPAVAAPTVPFPPPSSEQLKSGTASVVCLLNNFYPPKAVQWVDN 180  
 Db 181 ALOSGNSQESVTEQDSKSTYLSLSTLTLSKADYERHKYACEVTHQGLSSPVTAKSFNPG 240  
 QY 181 ALOSGNSQESVTEQDSKSTYLSLSTLTLSKADYERHKYACEVTHQGLSSPVTAKSFNPG 240  
 Db 241 EC 242  
 QY 241 EC 242  
 RESULT 3  
 ID US-09-234-182A-56 STANDAFC. PPT. 242 AA  
 XX xxxxxx  
 DE Sequence 56, Application US/08398613A  
 XX Sequence 56, Application US/08398613A  
 CC Patent No. 5677426  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Fong, Sherman  
 CC APPLICANT: Hebert, Caroline Alice  
 CC APPLICANT: Kim, Kyung Jin  
 CC APPLICANT: Leong, Steven R.  
 CC TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Infla  
 CC NUMBER OF SEQUENCES: 58  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Genentech, Inc.  
 CC STREET: 460 Point San Bruno Blvd  
 CC CITY: South San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94080  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: patin (Genentech)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/398,613A



CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Genentech, Inc  
 CC STREET: 460 Point San Bruno Blvd  
 CC CITY: South San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94080  
 CC  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: WinPatIn (Genentech)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/463,587A  
 CC FILING DATE: 05-Jun-1995  
 CC CLASSIFICATION: 435  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 08/050058  
 CC FILING DATE: 30-APR-1993  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US91/09133  
 CC FILING DATE: 03-DEC-1991  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/743614  
 CC FILING DATE: 09-AUG-1991  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/715300  
 CC FILING DATE: 14-JUN-1991  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/683400  
 CC FILING DATE: 10-APR-1991  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/621667  
 CC FILING DATE: 03-DEC-1990  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Schwartz, Timothy R.  
 CC REGISTRATION NUMBER: 33171  
 CC REFERENCE/DOCKET NUMBER: P0645F4D2  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415/225-7467  
 CC TELEFAX: 415/952-9881  
 CC TELEX: 910/371-7168  
 CC INFORMATION FOR SEQ ID NO: 25:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 237 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC  
 CC SEQUENCE 237 AA; 25977 MW; 322792 CN;

Query Match 85.8%; Score 1440; DB 2; Length 237;  
 Best Local Similarity 90.1%; Pred No 4 pae-qc;  
 Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;

Db 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGDVITTCRASQD-VN-TAVA- 57  
 QY 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGDVITTCRASQD-VN-TAVA- 60  
 Db 58 --WYQOKPKGKAPKLLIYKVSNEPFSVSPSGSGDFTLTITSSLPQEPATYVQSQH 115  
 QY 61 LHWYQOKPKGKAPKLLIYKVSNEPFSVSPSGSGDFTLTITSSLPQEPATYVQSQH 120  
 Db 116 TTPPTFGQGTKEIKETVAAPSEVIFPPSDGKLGSTASVGVTLNNFYPPKAVQWQVDN 175  
 QY 121 HVPITFGQGTKEIKETVAAPSEVIFPPSDGKLGSTASVGVTLNNFYPPKAVQWQVDN 180  
 Db 176 ALQSGNSQESVTEODSKOSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRG 235  
 QY 181 ALQSGNSQESVTEODSKOSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRG 240  
 Db 236 EC 237  
 QY 241 EC 242

RESULT 6  
 ID PCT-US91-09133-26 STANDARD: PPT: 237 AA.  
 XX  
 AC xxxxxx  
 XX  
 DT  
 XX  
 Sequence 26, Application PC/TUS9109133  
 XX  
 Sequence 26, Application PC/TUS9109133  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Genentech, Inc.  
 CC APPLICANT: Garrard, Lisa J.  
 CC APPLICANT: Hennen, Dennis J.  
 CC APPLICANT: Bass, Steven  
 CC APPLICANT: Greene, Ronald  
 CC APPLICANT: Lowman, Henry B.  
 CC APPLICANT: Wells, James A.  
 CC APPLICANT: Matthews, David J.  
 CC TITLE OF INVENTION: Enrichment Method For Variant Proteins  
 CC TITLE OF INVENTION: With Altered Binding Properties  
 CC NUMBER OF SEQUENCES: 27  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Genentech, Inc.  
 CC STREET: 460 Point San Bruno Blvd  
 CC CITY: South San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94080  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: patin (Genentech)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US91/09133  
 CC FILING DATE: 19911203  
 CC CLASSIFICATION: 425  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/743614  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/715300  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/683400  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/621667  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Benson, Robert H.  
 CC REGISTRATION NUMBER: 30,446  
 CC REFERENCE/DOCKET NUMBER: 645P4  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415/266-1489  
 CC TELEFAX: 415/952-9881  
 CC TELEX: 910/371-7168  
 CC INFORMATION FOR SEQ ID NO: 26:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 237 amino acids  
 CC TYPE: AMINO ACID  
 CC TOPOLOGY: linear  
 CC  
 CC SEQUENCE 237 AA; 25977 MW; 322792 CN;

Query Match 85.8%; Score 1440; DB 3; Length 237;  
 Best Local Similarity 90.1%; Pred. No. 4.88e-92;  
 Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;

Db 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGDVITTCRASQD-VN-TAVA- 57  
 QY 1 MKKNIAFLASMFVSIATNAYADIQMTQSPSSLSASVGDVITTCRASQD-VN-TAVA- 60  
 Db 58 --WYQOKPKGKAPKLLIYKVSNEPFSVSPSGSGDFTLTITSSLPQEPATYVQSQH 115  
 QY 61 LHWYQOKPKGKAPKLLIYKVSNEPFSVSPSGSGDFTLTITSSLPQEPATYVQSQH 120



CC REFERENCE/POCKET NUMBER: P1123  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 650/225-1489  
 CC TELEFAX: 650/225-1489  
 CC INFORMATION FOR SEQ ID NO: 17:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 218 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:  
 Query Match: 80.1%, Score 1345; DB 2; Length 218;  
 Best Local Similarity 90.9%; Pred. No. 3,07e-85;  
 Matches 199; Conservative 5; Mismatches 14; Indels 1; Gaps 1;  
 Db 1 DIQLTQSPSSLSASVGRVTITOPASRP-VDEGSDSYLNWYCKPKAPKLLIYAASYLE 59  
 24 DIQLTQSPSSLSASVGRVTITOPASRP-VDEGSDSYLNWYCKPKAPKLLIYAASYLE 83  
 60 SVPSPSSSSSSSTDTLTSSSQPEFAIYVCGQSHEDPTFGSTKVEIKETVAAPSV 119  
 84 SVPSPSSSSSSSTDTLTSSSQPEFAIYVCGQSHEDPTFGSTKVEIKETVAAPSV 143  
 120 FIFPSSDEQLKSTASVGLNNFYFPAKVWKVGNALSGNSQESVTEQDSKSTIYL 179  
 144 FIFPSSDEQLKSTASVGLNNFYFPAKVWKVGNALSGNSQESVTEQDSKSTIYL 203  
 180 SSTLSKADYKHKVYACEVTHQGLSSPVTKSPNPGEC 218  
 204 SSTLSKADYKHKVYACEVTHQGLSSPVTKSPNPGEC 242  
 RESULT 9  
 ID US-09-987-352B 19 STANDARD PFT: 218 AA.  
 XX  
 AC xxxxxx  
 CC  
 DT  
 DE Sequence 19, Application US/08887352B  
 XX Sequence 19, Application US/08887352B  
 CC Patent No. 5994511  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
 CC TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
 CC TITLE OF INVENTION: Improving Polypeptides  
 CC NUMBER OF SEQUENCES: 26  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Genentech, Inc.  
 CC STREET: 1 DNA Way  
 CC CITY: South San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94080  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: WinPatIn (Genentech)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/09/047,302F  
 CC FILING DATE: 03-Jul-1997  
 CC CLASSIFICATION: 530  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Svoboda, Craig G.  
 CC REGISTRATION NUMBER: 39,044  
 CC REFERENCE/POCKET NUMBER: P1123  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 650/225-1489  
 CC TELEFAX: 650/225-1489  
 CC INFORMATION FOR SEQ ID NO: 19:  
 CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 218 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:  
 Query Match: 80.1%, Score 1345; DB 2; Length 218;  
 Best Local Similarity 90.9%; Pred. No. 3,07e-85;  
 Matches 199; Conservative 5; Mismatches 14; Indels 1; Gaps 1;  
 Db 1 DIQLTQSPSSLSASVGRVTITOPASRP-VDEGSDSYLNWYCKPKAPKLLIYAASYLE 59  
 24 DIQLTQSPSSLSASVGRVTITOPASRP-VDEGSDSYLNWYCKPKAPKLLIYAASYLE 83  
 60 SVPSPSSSSSSSTDTLTSSSQPEFAIYVCGQSHEDPTFGSTKVEIKETVAAPSV 119  
 84 SVPSPSSSSSSSTDTLTSSSQPEFAIYVCGQSHEDPTFGSTKVEIKETVAAPSV 143  
 120 FIFPSSDEQLKSTASVGLNNFYFPAKVWKVGNALSGNSQESVTEQDSKSTIYL 179  
 144 FIFPSSDEQLKSTASVGLNNFYFPAKVWKVGNALSGNSQESVTEQDSKSTIYL 203  
 180 SSTLSKADYKHKVYACEVTHQGLSSPVTKSPNPGEC 218  
 204 SSTLSKADYKHKVYACEVTHQGLSSPVTKSPNPGEC 242  
 RESULT 10  
 ID US-09-987-352B 24 STANDARD PFT: 218 AA.  
 XX  
 AC xxxxxx  
 CC  
 DT  
 DE Sequence 24, Application US/08887352B  
 XX Sequence 24, Application US/08887352B  
 CC Patent No. 5994511  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
 CC TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
 CC TITLE OF INVENTION: Improving Polypeptides  
 CC NUMBER OF SEQUENCES: 26  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Genentech, Inc.  
 CC STREET: 1 DNA Way  
 CC CITY: South San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94080  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: WinPatIn (Genentech)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/887,352B  
 CC FILING DATE: 03-Jul-1997  
 CC CLASSIFICATION: 530  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Svoboda, Craig G.  
 CC REGISTRATION NUMBER: 39,044  
 CC REFERENCE/POCKET NUMBER: P1123  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 650/225-1489  
 CC TELEFAX: 650/225-1489  
 CC INFORMATION FOR SEQ ID NO: 24:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 218 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:  
 Query Match: 80.1%, Score 1345; DB 2; Length 218;





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24 210WGTGSSLSASVQCPWLTGTRSSSLVHG1ATYLVHWYKPKAPK...11FVSNPP 93
50 50APSPSSSSSSGIRFILLISSLAPPEFATYVQVQSNENPWTGAGTKVKPIVAAPSV 119
24 53WSPSSSSSSGIRFILLISSLAPPEFATYVQVQSNENPWTGAGTKVKPIVAAPSV 143
120 F1PSPSPKSTASVQVLLNNFPPPEAKYQKVKVNDALGSSNSVESVTEGSKSTSYL 179
244 F1PSPSSSLSSASVQVLLNNFPPPEAKYQKVKVNDALGSSNSVESVTEGSKSTSYL 203
180 SSTLLSKADYEHKVIYACIVTHQGISPPVTKEPSPDEC 218
224 SSTLLSKADYEHKVIYACIVTHQGISPPVTKEPSPDEC 242
Sequence 28, Application US/08398611A
Sequence 29, Application US/08398611A
Sequence 28, Application US/08398611A
Patent No. 5702946
GENERAL INFORMATION:
APPLICANT: Doershuik, Claire M.
APPLICANT: FCG, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,611A
FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOC#FT NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/325-5530
TELEFAX: 415/951-9881
TELEX: 910/371-7159
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE 28 37 AA, 25597 MW, 517516 DA.
Query Match
Best Local Similarity 81.4% Prod No 5 048-861
Matches 157 Conservative 12 Mismatches 21 Gaps 51

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[illegible]





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#authors      Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
               F.; Yamaki, S.; Kazi, H.; Takashi, I.; Shinoda, I.
#submission   submitted to JIPID, November 1998
#description   A new subgroup of k type light chains (VKV) identified in
               cases of AL amyloidosis.
#accession    JE0243
#molecule_type protein
#residues      1-215 #label ALI
SUMMARY       #length 215 #molecular-weight 23463 #checksum 78

Query Match    72.9%, Score 1224; DB 2; Length 215;
Best Local Similarity 82.3%; Pred. No. 9,10e-175;
Matches 181; Conservative 17; Mismatches 16; Indels 6; Gaps 4;

Db 1 EVLVTQSPATLSVSPGERATLS--VH---SN-LAWYQQRPGQAPRLIIYDASTPA 55
QY 24 DIQMTQSPSSLSASVGRVTITCRSSQSLVHGIGATYLVHWYQQRPGKAPKLLIYKVS 83
56 IGPAKFFSGSGSDTFLTISSLSQSELPALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 115
84 SGVPSRFSGSGSDTFLTISSLSQSELPALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 142
115 VFIPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSTYS 175
143 VFIPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSTYS 202
176 LSSTLTSKADYEKKHVVACEVTHQGLSSPVTKSNRQEC 215
203 LSSTLTSKADYEKKHVVACEVTHQGLSSPVTKSNRQEC 242

RESULT 3
ENTRY    JE0243 #type complete
TITLE    Ig kappa chain N193 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
05-Dec-1998

ACCESSIONS
REFERENCE JE0243
#authors  Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
           F.; Yamaki, S.; Kazi, H.; Takashi, I.; Shinoda, I.
#submission submitted to JIPID, November 1998
#description A new subgroup of k type light chains (VKV) identified in
           cases of AL amyloidosis.
#accession JE0243
#molecule_type protein
#residues 1-215 #label ALI
SUMMARY #length 215 #molecular-weight 23455 #checksum 947

Query Match    70.4%, Score 1182; DB 2; Length 215;
Best Local Similarity 81.4%; Pred. No. 8,30e-168;
Matches 179; Conservative 15; Mismatches 20; Indels 6; Gaps 3;

Db 1 EIVMTQSPATLSVSPGERATLS--V----ATNVWVMQKLGQAPRLIIYDASTPA 55
QY 24 DIQMTQSPSSLSASVGRVTITCRSSQSLVHGIGATYLVHWYQQRPGKAPKLLIYKVS 83
56 IGPAKFFSGSGSDTFLTISSLSQSELPALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 115
84 SGVPSRFSGSGSDTFLTISSLSQSELPALYYCQYNTWPLTFGSGTKVEIKRTVAAPS 142
115 VFIPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSTYS 175
143 VFIPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSTYS 202
176 LSSTLTSKADYEKKHVVACEVTHQGLSSPVTKSNRQEC 215
203 LSSTLTSKADYEKKHVVACEVTHQGLSSPVTKSNRQEC 242

RESULT 4
ENTRY    A23746 #type complete
TITLE    Ig kappa chain V-III (KAP cold agglutinin) - human

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#formal_name Homo sapiens #common_name man
#sequence_revision 30-Dec-1991 #text_change
16-Aug-1996
ACCESSIONS
REFERENCE A23746
#authors  Leonil, J.; Ghiso, J.; Goni, F.; Frangione, B.
           J. Biol. Chem. (1991) 266:2836-2842
#journal   The primary structure of the Fab fragment of protein KAP, a
           monoclonal immunoglobulin M cold agglutinin.
#cross-references MUID:91131575
#accession A23746 Preliminary
#status     1-215 #label LEO
#molecule_type protein
#residues   heterotetramer: immunoglobulin
           #length 215 #molecular-weight 23050 #checksum 116

Query Match    68.0%, Score 1142; DB 2; Length 215;
Best Local Similarity 78.9%; Pred. No. 3,46e-161;
Matches 172; Conservative 19; Mismatches 23; Indels 4; Gaps 2;

Db 1 EIVLTQSPATLSVSPGERATLS--GGAS--QSVSSNYLAWYQQRPGQAPRLIIYDASSRA 56
QY 24 DIQMTQSPSSLSASVGRVTITCRSSQSLVHGIGATYLVHWYQQRPGKAPKLLIYKVS 83
57 TGIPRFSGSGSDTFLTISSLEPEDFAYVYQYQYSSPLTFGGGKVEIKRTVAAPS 116
84 SGVPSRFSGSGSDTFLTISSLEPEDFAYVYQYQYSSPLTFGGGKVEIKRTVAAPS 143
117 FIFPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSTYS 176
144 FIFPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSTYS 203
177 SSTLTSKADYEKKHVVAGEVTHQGLSSPVTKSNRGE 214
204 SSTLTSKADYEKKHVVAGEVTHQGLSSPVTKSNRGE 241

RESULT 5
ENTRY    JE0241 #type complete
TITLE    Ig kappa chain Am37 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
05-Dec-1998

ACCESSIONS
REFERENCE JE0241
#authors  Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima,
           M.; Takashi, I.; Shinoda, I.
#submission submitted to JIPID, November 1998
#description Structure relationship of kappa type light chains with AL
           amyloidosis: Multiple deletions found in a VKV protein.
#accession JE0241
#molecule_type protein
#residues 1-216 #label ALI
SUMMARY #length 216 #molecular-weight 23926 #checksum 4962

Query Match    67.3%, Score 1130; DB 2; Length 216;
Best Local Similarity 77.2%; Pred. No. 3,33e-159;
Matches 169; Conservative 15; Mismatches 32; Indels 3; Gaps 3;

Db 1 DIVLTQSPDFLAVSLGEPATINCKSSQSVLYN-SKNFLAWYQQRPGQ-PKLLIW-ANVRE 57
QY 24 DIQMTQSPSSLSASVGRVTITCRSSQSLVHGIGATYLVHWYQQRPGKAPKLLIYKVS 83
58 SGVPSRFSGSGSDTFLTISSLNCAELVAVVYQYQYVSTVPSFGGQPIRIKRTVAAPS 117
84 SGVPSRFSGSGSDTFLTISSLNCAELVAVVYQYQYVSTVPSFGGQPIRIKRTVAAPS 143
118 FIFPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSTYS 177
144 FIFPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNALSGNSQESVTFQDSKSTYS 203
178 SSTLTSKADYEKKHVVAGEVTHQGLSSPVTKSNRQEC 216

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RESULT 2
ID Q9YAVC PRELIMINARY: PRT: 397 AA.
AC Q9YAVC
DI 01-NOV-1999 (TREMblrel. 12, Created)
DI 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DI 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE DJ576H34.2 (SIRP-BETA1) (SIGNAL REGULATOR PROTEIN RPTA 1)
GN DJ576H34.2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN
RP
RQ SEQUENCE FROM N.A.
RA MATTHEWS L.
RC Submitted (JUN-1999) to the EMBL/GenBank/TrfJ databases
DR EMBL: AL049634; CAB46661.1;
SQ SEQUENCE 397 AA: 43037 MW: 9581105 CAC32;
Query Match 13.7% Score 230; DB 4; Length 397;
Best Local Similarity 26.6%; Pred No. 1 50e-24;
Matches 61; Conservative 64; Mismatches 87; Indels 21; Gaps 20;
DB 18 PELLTLLDGLDVAAGSELEWIPKESVSVAAAGESATLFTAMTSIFVSPFM-WFF 60
UY 5 AELLASMPVESIAINAYADIQMIQSPSSLSASVGLRVLITPSSQSLVHGIGATYCHWD 65
DB 69 G-AG-AGRELINQVEGHPPTVTVSELTAKNNLDFTSISNTPADAGTYVQVWYKGS 126
CY 65 LKPKAFKLLIKVEN-RFSGVPSRFSSGSGT-DFTLTSSLOPEDFATYVQVWYKGS 122
DB 127 PDEVEKSGAGTELSVPAKPSAPV-VSGPAAPATPQHTVSTTCSHSPSPDITLKWFKN 195
QY 123 P-LFPGQTKVEIK-PTVAAPSVETFPSSSLASVGLRVLITPSSQSLVHGIGATYCHWD 178
DI 180 DRELK-ETFINV-EPASLSVSYSHSHARVWVTFDQVHS-V-ICETATITL 223
QY 179 DVALSSGNSGSEVHSGWQSEYSL-SST-LTISKAVYFVAVVAVETVHGL 229
RESULT 3
ID P78224 PRELIMINARY: PRT: 503 AA
AC P78224, 500082,
DI 01-NOV-1999 (TREMblrel. 08, Created)
DI 01-NOV-1999 (TREMblrel. 08, Last sequence update)
DI 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1, PRECURSOR
(SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SHPS-1) (SIGNAL-
REGULATOR PROTEIN ALPHA-1) (SIRP-ALPHA1) (MYD-1 ANTIGEN).
P1PNS1 OR SHPS-1 OR DJ684024.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN
RP
RQ SEQUENCE FROM N.A.
RA
RQ TISSUE-BRAIN:
RX MEDLINE: 9722399.
PA YAMAGI Y., MATOZAKI I., AMANO Y., MATSUDA Y., TAKAHASHI N., OCHI F.,
RA FUJIOKA Y., KASUGA M.,
RI "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
RI localization of genes."
RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN
RQ SEQUENCE FROM N.A.
RA
RQ TISSUE-PLACENTA:
RX MEDLINE: 97215901.
PA KASITCHENKOVA A., CHEN Z., SUPES I., WANG H., SCHILLING I.,
RA ULLRICH A.,
RI "A family of proteins that inhibit signalling through tyrosine kinase
RI receptors."
RL Nature 396:191-196(1997).
RN
RQ SEQUENCE OF 146-503 FROM N.A.
RA

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PL Submitted (MAR-1999) to the EMBL/GenBank/TrfJ databases
AC 1- FUNCTION, BINDS TO THE SH2 DOMAINS OF PROTEIN TYROSINE PHOSPHATASE
CC 2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS
CC MITOGENS AND CELL ADHESION. MAY ACT AS A DOCKING PROTEIN AND
CC INDUCE TRANSLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA
CC MEMBRANE.
CC 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC 1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN BRAIN,
CC HIGH LEVELS ALSO PRESENT IN HEART, SPLEEN, TESTIS, OVARY AND
CC PERIPHERAL BLOOD LEUKOCYTES.
CC 1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC TWO C1-LIKE AND ONE V-LIKE DOMAINS.
DR EMBL: D86643; BAA12974.1;
DR EMBL: Y10375; CAA71403.1;
DR EMBL: AL034562; CAB38874.1;
DR MIM: 602461;
DP PFAM: PF00047; Ig: 3.
KW Signal; Transmembrane; Alternative splicing; Immunoglobulin domain;
KW Glycoprotein; SH2-binding; Phosphorylation.
FT SIGNAL 1 26
FT CHAIN 27 503
FT DOMAIN 27 372
FT TRANSMEM 373 393
FT DOMAIN 394 503
FT DOMAIN 43 129
FT DOMAIN 164 233
FT DOMAIN 266 339
FT DOMAIN 428 431
FT DOMAIN 438 443
FT DOMAIN 452 455
FT DOMAIN 469 472
FT DOMAIN 495 498
FT MOD_RES 428 428
FT MOD_RES 452 452
FT MOD_RES 459 459
FT MOD_RES 495 495
FT CARBOHYD 244 244
FT CARBOHYD 269 269
FT CARBOHYD 291 291
FT CARBOHYD 318 318
FT SEQUENCE 503 AA: 54812 MW: 5642727 ZP032;
Query Match 13.6% Score 229; DB 4; Length 503;
Best Local Similarity 26.6%; Pred No. 1 50e-24;
Matches 61; Conservative 58; Mismatches 93; Indels 17; Gaps 16;
DB 17 LLAASCAWSVAGE-EELQVIFDKSVSVAAAGESAILHCTV-SLIP-VGP--IQWPG 71
QY 7 PLLASMFVSIATNAYADIQMTSPSSLSASVGLRVLITPSSQSLVHGIGATYCHWD 66
DB 72 -AG-PAPELYNQVEGHPPTVTVSELTAKNNLDFTSISNTPADAGTYVQVWYKGS 129
QY 67 KFGKAPKLLIKVEN-RFSGVPSRFSSGSGT-DFTLTSSLOPEDFATYVQVWYKGS 123
DB 130 DTEPKSGAGTELSVPAKPSAPV-VSGPAAPATPQHTVSTTCSHSPSPDITLKWFKN 188
QY 124 LT-FGQTKVEIK-PTVAAPSVETFPSSSLASVGLRVLITPSSQSLVHGIGATYCHWD 180
DB 189 EL-S-DEQTNV-DPVGESVSYSHSHARVWVTFDQVHSQVCEVAHVTL 234
QY 181 ALQSGNSGSEVTEGDSKDSYSLSSLTLSKADYERKRVACEVTHQGL 229
RESULT 4
ID Q00241 PRELIMINARY: PRT: 398 AA
AC Q00241;
DI 01-NOV-1998 (TREMblrel. 08, Created)
DI 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DI 01-AUG-1999 (TREMblrel. 11, Last annotation update)
DE SIGNAL-REGULATOR PROTEIN BETA-1 PRECURSOR (SIRP-BETA1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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CC the complementarity determining regions (CDRs) of murine anti-IL-8  
 CC antibody 634.2.5 (see W69309) light chain within a human 6-subgroup  
 CC 1 light chain template. Humanised anti-IL-8 monoclonal antibodies  
 CC (WABs) and variants are described for use in diagnostic applications  
 CC and in the treatment of inflammatory disorders. The invention  
 CC provides conjugates of an antibody fragment and a non-proteinaceous  
 CC polymer, such as PEG, that have improved half-life, mean residence  
 CC time, and/or clearance rate compared to non-derivatised parental  
 CC antibody fragment. Also claimed are a polypeptide that is an  
 CC acid sequence comprising the light chain CDRs of 664V11M35E, a  
 CC nucleic acid encoding such a polypeptide, and a method of producing  
 CC the polypeptide in host cells. The conjugates can be used for  
 CC immune therapy of inflammatory disorders, e.g. psoriasis, responses  
 CC associated with inflammatory bowel disease (such as Crohn's disease  
 CC and ulcerative colitis), ischemic reperfusion, adult respiratory  
 CC distress syndrome, dermatitis, meningitis, encephalitis, uveitis,  
 CC autoimmune diseases such as rheumatoid arthritis, Sjorgen's  
 CC syndrome, vasculitis, diseases involving leukocyte diapedesis,  
 CC central nervous system inflammatory disorder, multiple organ injury  
 CC syndrome secondary to septicemia or trauma, alcoholic hepatitis,  
 CC bacterial pneumonia, antigen-antibody complex mediated diseases,  
 CC inflammations of the lung, including pleurisy, alveolitis,  
 CC vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and  
 CC cystic fibrosis. They can also be used in diagnostic applications.  
 CC Sequence 242 AA;

Query Match 99.7% Score 1076 DB 1 Length 242;  
 Best Local Similarity 99.6% Pred. No. 2,110-117;  
 Matches 241: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTVITCRSSSLVHGIGNTY 60  
 QY 1 MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTVITCRSSSLVHGIGNTY 60  
 Db 61 LHWYQKPKGAPKLLIYKVNPFSGVSPFSGSGSGTDFTLTSSLPQEPFATYVQSQT 120  
 QY 61 LHWYQKPKGAPKLLIYKVNPFSGVSPFSGSGSGTDFTLTSSLPQEPFATYVQSQT 120  
 Db 121 HVPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRFAKVQWKVDN 180  
 QY 121 HVPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRFAKVQWKVDN 180  
 Db 181 ALQSGNSQESVTEQDSKDTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNFG 240  
 QY 181 ALQSGNSQESVTEQDSKDTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNFG 240  
 Db 241 EC 242  
 QY 241 EC 242

RESULT 2 standard; Protein: 242 AA.  
 ID W69313;  
 AC W69313;  
 DE 15-FEB-1999 (first entry)  
 DE Anti-IL-8 humanised antibody 664V11M35A.F(ab')2.  
 KW Humanised antibody; chimeric antibody; monoclonal antibody; mouse;  
 KW human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;  
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW ischaemic reperfusion; adult respiratory distress syndrome;  
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;  
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;  
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;  
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;  
 KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;  
 KW therapy; 664V11M35A.F(ab')2.  
 OS Chimeric - Mus sp.  
 OS Chimeric - Homo sapiens.  
 FT Key Location/Qualifiers  
 FT CDS 439..1167  
 FT /\*tag=a  
 PN W09837200-A2.

PD 27-AUG-1998.  
 PF 20-FEB-1998: U03337.  
 PR 22-JAN-1998: US-012115.  
 PR 21-FEB-1997: US-804444.  
 PA (GETH) GENENTECH INC.  
 PI Hsueh V. Koumenis I, Leong SP, Presta LP, Shahrokh Z, Scalet A, J  
 PI Zapata GA;  
 DR WPI: 98-467563/40.  
 DR N-P8DB; V44953.  
 PT New conjugates of antibody fragments - having covalently attached  
 PT non-proteinaceous polymer molecules, particularly polyethylene  
 PT glycol, for improving the residence time in the circulation.  
 PS Example K, Fig 4B-D; 328pp; English.  
 CC This is the amino acid sequence of a polypeptide encoded by  
 CC plasmid p664V11M35A.F(ab')2 (see V44953) comprising a murine-human  
 CC chimeric Fab containing complementarity determining regions of  
 CC murine anti-interleukin-8 (IL-8) monoclonal antibody (WAB) 634.2.5  
 CC (see W69309-10) in a human template. Humanised anti-IL-8 MABs (see  
 CC W69301-04) are described for use in diagnostic applications and in  
 CC the treatment of inflammatory disorders. The invention provides  
 CC conjugates of an antibody fragment and a polymer, such as PEG, that  
 CC have improved half-life, mean residence time, and/or clearance rate.  
 CC The conjugates can be used for immune therapy of e.g. psoriasis,  
 CC responses associated with inflammatory bowel disease (such as  
 CC Crohn's disease and ulcerative colitis), ischemic reperfusion,  
 CC adult respiratory distress syndrome, dermatitis, meningitis,  
 CC encephalitis, uveitis, autoimmune diseases such as rheumatoid  
 CC arthritis, Sjorgen's syndrome, vasculitis, diseases involving  
 CC leukocyte diapedesis, central nervous system inflammatory disorder,  
 CC multiple organ injury syndrome secondary to septicemia or trauma,  
 CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex  
 CC mediated diseases, inflammations of the lung, including pleurisy,  
 CC alveolitis, vasculitis, pneumonia, chronic bronchitis,  
 CC bronchiectasis, and cystic fibrosis.  
 CC Sequence 242 AA;

Query Match 99.6% Score 1675; DB 1 Length 242;  
 Best Local Similarity 99.6% Pred. No. 2,140-117;  
 Matches 241: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTVITCRSSSLVHGIGNTY 60  
 QY 1 MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTVITCRSSSLVHGIGNTY 60  
 Db 61 LHWYQKPKGAPKLLIYKVNPFSGVSPFSGSGSGTDFTLTSSLPQEPFATYVQSQT 120  
 QY 61 LHWYQKPKGAPKLLIYKVNPFSGVSPFSGSGSGTDFTLTSSLPQEPFATYVQSQT 120  
 Db 121 HVPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRFAKVQWKVDN 180  
 QY 121 HVPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRFAKVQWKVDN 180  
 Db 181 ALQSGNSQESVTEQDSKDTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNFG 240  
 QY 181 ALQSGNSQESVTEQDSKDTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNFG 240  
 Db 241 EC 242  
 QY 241 EC 242

RESULT 3 standard; Protein: 242 AA.  
 ID W69301;  
 AC W69301;  
 DE 15-FEB-1999 (first entry)  
 DE Humanised anti-IL-8 664.2.5V11M35A light chain.  
 KW Humanised antibody; monoclonal antibody; interleukin-8;  
 KW inflammation; immunotherapy; therapy; psoriasis;  
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW ischaemic reperfusion; adult respiratory distress syndrome;  
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;  
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;  
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;



SC Sequence 242 AA.

Query Match 89.9% Score 1511; DB 1; Length 242;  
Rest Local Similarity 87.6%; Pred No 1 38e-104;  
Matches 222, Conservative 19, Mismatches 12, Indels 0, Gaps 0.

DE 1 MKKNIAPFLASMFVSIATNAYADIVMTPTLSPLVSLGQASISCRSSQSLVHGIGNTY 60  
QY 1 MKKNIAPFLASMFVSIATNAYADIVMTPTLSPLVSLGQASISCRSSQSLVHGIGNTY 60

DE 61 LHWYLOKPGOSKLLLYKVSNPFSVGPDPSPSGSGGTDFLTPSPVEADLGLVFCQSST 120  
QY 61 LHWYLOKPGOSKLLLYKVSNPFSVGPDPSPSGSGGTDFLTPSPVEADLGLVFCQSST 120

DE 121 HVPITFGAGTKLEIKPAVAAPTIFIPPPSSQSLKSGTASVVCLLNNFYPPFAKVMQKVDN 180  
QY 121 HVPITFGAGTKLEIKPAVAAPTIFIPPPSSQSLKSGTASVVCLLNNFYPPFAKVMQKVDN 180

DE 181 ALQSGNSQESVTEQDSKSTYSLSSTILSKADYKHKVYACEVTHAGLSPPVTKSFNPG 240  
QY 181 ALQSGNSQESVTEQDSKSTYSLSSTILSKADYKHKVYACEVTHAGLSPPVTKSFNPG 240

DE 241 EC 242  
QY 241 EC 242

RESULT 5  
ID W42323 standard; Protein: 242 AA.  
AC W42323;  
DI 15-APR-1998 (first entry)  
DE Murine variable region and human constant region light chain sequence.  
KW Light chain: heavy chain; monoclonal antibody: Interleukin-8; IL-8;  
KW Inflammatory disorder; bacterial pneumonia; neutrophil chemotaxis;  
KW anti IL-8 monoclonal antibody; IL-8 mediated elastase release;  
KW Streptococcus pneumoniae; Escherichia coli; Pseudomonas aeruginosa;  
KW ulcerative colitis.  
OS Chimeric - Mus sp.  
FH Chimeric - Homo sapiens.  
FT Key Location/Qualifiers  
FT Peptide 1..23  
FT Region /note= "signal peptide"  
FT Region 1..114  
FT Region /note= "murine variable light region"  
FT Region 115..219  
FT Region /note= "human constant light region"  
FT Region 47..62  
FT Region /note= "complementarity determining region (CDR) as indicated by Kabat sequence comparison"  
FT Region 49..60  
FT Region /note= "complementarity determining region (CDR) as indicated by X-ray crystallography"  
FT Region 78..84  
FT Region /note= "complementarity determining region (CDR) as indicated by Kabat sequence comparison"  
FT Region 78..80  
FT Region /note= "complementarity determining region (CDR) as indicated by X-ray crystallography"  
FT Region 117..125  
FT Region /note= "complementarity determining region (CDR) as indicated by Kabat sequence comparison"  
FT Region 119..124  
FT Region /note= "complementarity determining region (CDR) as indicated by X-ray crystallography"  
US5686070-A.  
PD 11-NOV-1997.  
DE 01-MAR-1995; 398612.  
PR 01-MAR-1995; US-598612.  
PA 03-MAR-1994; US-205964.  
PA (GEN) GENENTECH INC.  
PA (INDV) UNIV INDIANA.  
PI Doerschuk CM, Fogg S, Hebert CA, Kim KJ, Leong SP.  
DR WPI: 97-558085/51

DE N-PSDB: V03226.  
FT Treatment of bacterial pneumonia - with monoclonal antibody specific for interleukin-8; inhibits lung inflammatory conditions  
FS Disclosure; Fig 27, 63pp; English.  
CC The present sequence represents the sequence for murine monoclonal antibody 6G4.2.5 light chain variable region and a human light chain constant region. The 6G4.2.5 antibody is an anti rabbit interleukin-8 (IL-8) antibody. IL-8 is a neutrophil chemotactic peptide secreted by a variety of cells in response to inflammatory mediators. IL-8 can play an important role in the pathogenesis of inflammatory disorders such as adult respiratory distress syndrome (ARDS), septic shock and multiple organ failure. Treatment of bacterial pneumonia in a mammal comprises administering an anti IL-8 monoclonal antibody, such as, e.g. humanised 6G4.2.5, that binds human IL-8 with a KD of 10-8 to 10-11 M, inhibits neutrophil chemotaxis in response to IL-8, inhibits IL-8 mediated elastase release by neutrophils and does not bind to C5a, beta-TG or platelet factor 4. IL-8 specific monoclonal antibodies are especially for treating pneumonia caused by Streptococcus pneumoniae, E. coli or Pseudomonas aeruginosa in humans. The antibodies may also be used in the treatment of ulcerative colitis and other inflammatory conditions.  
CC Inflammatory conditions.  
SQ Sequence 242 AA;

Query Match 89.9% Score 1511; DB 1; Length 242;  
Rest Local Similarity 87.6%; Pred No 1 38e-104;  
Matches 222, Conservative 18, Mismatches 12, Indels 0, Gaps 0;

DE 1 MKKNIAPFLASMFVSIATNAYADIVMTPTLSPLVSLGQASISCRSSQSLVHGIGNTY 60  
QY 1 MKKNIAPFLASMFVSIATNAYADIVMTPTLSPLVSLGQASISCRSSQSLVHGIGNTY 60

DE 61 LHWYLOKPGOSKLLLYKVSNPFSVGPDPSPSGSGGTDFLTPSPVEADLGLVFCQSST 120  
QY 61 LHWYLOKPGOSKLLLYKVSNPFSVGPDPSPSGSGGTDFLTPSPVEADLGLVFCQSST 120

DE 121 HVPITFGAGTKLEIKPAVAAPTIFIPPPSSQSLKSGTASVVCLLNNFYPPFAKVMQKVDN 180  
QY 121 HVPITFGAGTKLEIKPAVAAPTIFIPPPSSQSLKSGTASVVCLLNNFYPPFAKVMQKVDN 180

DE 181 ALQSGNSQESVTEQDSKSTYSLSSTILSKADYKHKVYACEVTHAGLSPPVTKSFNPG 240  
QY 181 ALQSGNSQESVTEQDSKSTYSLSSTILSKADYKHKVYACEVTHAGLSPPVTKSFNPG 240

DE 241 EC 242  
QY 241 EC 242

RESULT 6  
ID R86323 standard; Protein: 242 AA.  
AC R86323;  
DI 12-MAR-1996 (first entry)  
DE Chimeric 6G4.2.5 light chain.  
KW Monoclonal antibody 6G4.2.5; MAb, interleukin-8; IL-8.  
KW Chimeric antibody; Fab; antibody engineering; inflammation;  
KW inflammatory bowel disease; ulcerative colitis; bacterial pneumonia.  
OS Chimeric Mus sp.;  
OS Chimeric Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..23  
FT Region /label= "sig peptide"  
FT Region /note= "still signal peptide"  
FT Region 24..137  
FT Region /label= "VL region"  
FT Region /note= "murine light chain variable region"  
FT Region 47..63  
FT Region /label= "CDP-1"  
FT Region /note= "CDP-1 location determined by Kabat sequence comparison; amino acids 49-59 constitute CDR-1 determined by X-ray crystallography"  
FT Region 78..84  
FT Region /label= "CDP-2"









RESULT 11  
 ID W05622 standard; Protein: 237 AA.  
 AC W05622:  
 DT 08-JUN-1999 (first entry)  
 DE PS130 expression cassette encoded rhumab CD18 light chain  
 KW Murine anti-CD18 antibody, heavy chain, humanized; myocardial infarction;  
 KW Burns; thermal injury; ischemic shock; ischaemic haemorrhagic;  
 KW Hemorrhagic; stroke; light chain  
 OS Mus musculus.  
 PS Synthetic.  
 FH Key Location/Qualifiers  
 FT SId peptide 1..23  
 PN W09856418-A1.  
 PD 17-DEC-1998.  
 PE 12-JUN-1999: 012209.  
 PR 13-JUN-1997: US-874897.  
 PA (GETH) GENENTECH INC.  
 BA Wang XM, Oeswein JO, Ongpipattanakul B, Shahrokh Z,  
 DR Wang SX, Weissburg RP, Wong RL;  
 WPI: 99-08966/07.  
 PT New stable aqueous antibody formulations - comprising an antibody  
 PT not subjected to lyophilisation, a buffer maintaining the pH at 4.5  
 PI - 5, a surfactant and a polyol  
 PS Disclosure: Fig 21A; 87pp; English.  
 CC The sequence is that of the PS130 encoded light chain of a humanized  
 CC murine anti-CD18 antibody rhumab CD18. It can be used for the treatment  
 CC of disorders which include haemorrhagic shock, thermal injury (such  
 CC as that resulting from burns), stroke (including ischaemic and  
 CC haemorrhagic stroke) and myocardial infarction. The antibody  
 CC formulation can be stabilised at a temperature of 2-8 deg. C  
 CC for at least one year or at a temperature of 30 deg. C for at  
 CC least one month and is stable following freezing and thawing.  
 SQ Sequence 237 AA;  
 Query Match 87.0%; Score 1462; DB 1; Length 237;  
 Best Local Similarity 90.9%; Pred. No. 8,630-101;  
 Matches 220; Conservative 6; Mismatches 11; Idels 5; Gaps 2;  
 Db 1 MKKNIAPLLASMEVFSTATNAYADIOMTQSPSSLSASVGRVITICRASQD---INN-Y 55  
 QY 1 MKKNIAPLLASMEVFSTATNAYADIOMTQSPSSLSASVGRVITICRASQSLVHGIGET 60  
 Db 56 LNWYQKPKAPKLLIYVTSILHSGVSPFSRSGSGTCTYLTIISSLOPEDFATYVCOGN 115  
 QY 61 LHWYQKPKAPKLLIYKVSNNRFSVGRVITICRASQSLVHGIGET 60  
 Db 115 TLPTTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWVDN 175  
 QY 121 HVLPTFGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWVDN 180  
 Db 175 ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSSPVTKSFNRG 235  
 QY 181 ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSSPVTKSFNRG 240  
 Db 236 EC 237  
 QY 241 EC 242  
 RESULT 12  
 ID W05634 standard; protein: 237 AA.  
 AC W05634:  
 DT 06-APR-1999 (first entry)  
 DE Recombinant humanised anti-CD18 antibody rhumab CD18 light chain.  
 KW Recombinant humanised anti-CD18 antibody; rhumab CD18; leucine zipper;  
 KW murine monoclonal antibody; muMAB H52; protein recovery; filtration;  
 KW chromatography.  
 OS Mus sp.  
 PS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..23

FT W09856808-A1.  
 PN 17-DEC-1998.  
 PE 12-JUN-1998: U12334.  
 PR 13-JUN-1997: US-050951.  
 PA (GETH) GENENTECH INC  
 PI Blank GS, Narindray DS, Zapata GA;  
 DR WPI: 99-060267/05.  
 DR N-PSDB: X03840.  
 PT New method for recovering polypeptides from cell cultures - by  
 PT treating with reagent and filtering to remove reagent  
 PS Example, Fig 4; 43pp; English.  
 CC A method has been developed for recovering a polypeptide comprising: (a)  
 CC exposing a composition comprising a polypeptide to a reagent which binds  
 CC to or modifies the polypeptide, where the reagent is immobilized on a  
 CC solid phase; and (b) passing the composition through a filter bearing an  
 CC opposite charge to the reagent so as to remove leached reagent from the  
 CC composition. The present invention also describes a method for modifying  
 CC a precursor antibody comprising a leucine zipper by exposing the  
 CC precursor antibody to a protease immobilized on a solid support so that  
 CC the protease removes the zipper. The methods can be used to purify  
 CC proteins from cell cultures. They are especially useful for isolating  
 CC antibodies. The methods overcome the problem of reagent leakage into the  
 CC protein as is the case in prior art immobilized modification systems. By  
 CC using a opposite charge filter the reagent can be excluded from the  
 CC sample, preventing contamination. The present sequence represents the  
 CC recombinant humanised anti-CD18 antibody (rhMAB CD18) light chain,  
 CC which is used in an example from the present invention.  
 SQ Sequence 237 AA;  
 Query Match 87.0%; Score 1462; DB 1; Length 237;  
 Best Local Similarity 90.9%; Pred. No. 8,630-101;  
 Matches 220; Conservative 6; Mismatches 11; Idels 5; Gaps 2;  
 Db 1 MKKNIAPLLASMEVFSTATNAYADIOMTQSPSSLSASVGRVITICRASQD---INN-Y 55  
 QY 1 MKKNIAPLLASMEVFSTATNAYADIOMTQSPSSLSASVGRVITICRASQSLVHGIGET 60  
 Db 56 LNWYQKPKAPKLLIYVTSILHSGVSPFSRSGSGTCTYLTIISSLOPEDFATYVCOGN 115  
 QY 61 LHWYQKPKAPKLLIYKVSNNRFSVGRVITICRASQSLVHGIGET 60  
 Db 115 TLPTTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWVDN 175  
 QY 121 HVLPTFGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWVDN 180  
 Db 175 ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSSPVTKSFNRG 235  
 QY 181 ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSSPVTKSFNRG 240  
 Db 236 EC 237  
 QY 241 EC 242  
 RESULT 13  
 ID W07073 standard; Protein: 237 AA.  
 AC W07073:  
 DT 27-JAN-1999 (first entry)  
 DE Protein encoded by Fab-display antibody vector pMB4-19-1.6.  
 KW Murine; humanised antibody; VEGF-induced angiogenesis; tumour;  
 KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;  
 KW retinal disorder; age-related macular degeneration; diabetic retinopathy;  
 KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.  
 OS Synthetic.  
 PN W09845331-A2.  
 PD 15-OCT-1998.  
 PE 03-APP-1998: 006604  
 PR 06-AUG-1997: US-908469.  
 PR 07-APR-1997: US-833504.  
 PA (GETH) GENENTECH INC.  
 PI Baca M, Chen YM, Lowman HB, Presta LG, Wells JA;  
 DR WPI: 98-568337/48.

13 N-180, W-474.  
 14 New humanised antibody with affinity for vascular endothelial growth  
 15 factor (VEGF) for treatment of tumours, retinal disease and other  
 16 angiogenic states, also related nucleic acid, vectors and  
 17 transformed cells.  
 18 Example in Fig 8A-E: 100pp; English.  
 19 The present invention is directed to the Fab displaying antibody vector  
 20 (pMDL-1.1b), which is used in the course of the invention. The  
 21 specification describes humanised murine anti-vascular endothelial  
 22 growth factor (anti-VEGF) antibodies. The humanised antibodies  
 23 are used to inhibit VEGF induced angiogenesis, particularly for treating  
 24 or preventing tumours (of any type) and retinal disorders (e.g. age  
 25 related macular degeneration, diabetic retinopathy). They can also be  
 26 used to treat other conditions that involve angiogenesis, e.g. rheumatoid  
 27 arthritis, psoriasis, osteoarthritis, Grave's disease, etc.  
 28 Sequence: 237 AA:  
 29  
 30 Query Match: 86.1%; Score 1451; DB 1; Length 237;  
 31 Best local Similarity: 90.1%; Pred No 6.13e-169;  
 32 Matches: 219; Conservative: 9; Mismatches: 9; Indels: 5; Gaps: 4;  
 33  
 34 1 MKKNIAFLASMEVFSTAINAYADTQLTQSPSSLSASVGRVITTC-SA-S--QDIN-Y 55  
 35 1 MKKNIAFLASMEVFSTAINAYADTQLTQSPSSLSASVGRVITTCQSSSLVHGIGETY 60  
 36 56 LHWYKPKKAKPKKIIYSASELYSEVSPSPSSSSSGSDIFITLSSLPEDFAITYQDSI 115  
 37 61 LHWYKPKKAKPKKIIYSASELYSEVSPSPSSSSSGSDIFITLSSLPEDFAITYQDSI 120  
 38 116 TVWVDTGDTKVKETPAARSVFPPSPDEGLKSGTASVCLNNYFPRAKQWQVDN 175  
 39 121 HWVLTGGQTKVETPAARSVFPPSPDEGLKSGTASVCLNNYFPRAKQWQVDN 180  
 40 176 ALQSNSSQSVTFDESKTSTYSLSSITLTKADYKPKKVVVA-TVHUNLSSSVKPSNRG 235  
 41 181 ALQSNSSQSVTFDESKTSTYSLSSITLTKADYKPKKVVVA-TVHUNLSSSVKPSNRG 240  
 42 236 EC 237  
 43 241 EC 242  
 44  
 45 RESULT: 15  
 46 ID W83493 standard; Protein: 698 AA.  
 47 AC W83493;  
 48 DI 08-MAR-1999 (first entry)  
 49 DE 415 Fab molecule expressed on a phagemid surface.  
 50 KW Human: growth hormone; hGH; phagemid particle; enzyme substrate;  
 51 FN fusion gene; phage; protein coat.  
 52 OS Homo sapiens.  
 53 GS Synthetic.  
 54 PN US5846765-A.  
 55 PD 08-DEC-1998.  
 56 PF 16-MAY-1995; 441871.  
 57 PR 03-DEC-1993; US-161692.  
 58 PR 03-DEC-1990; US-621667.  
 59 PR 10-APR-1991; US-683400.  
 60 PR 14-JUN-1991; US-715300.  
 61 PR 09-AUG-1991; US-743614.  
 62 PR 03-DEC-1991; WO-009133.  
 63 PR 06-APR-1993; US-864452.  
 64 PR 30-APR-1993; US-050058.  
 65 PR 05-APR-1995; US-418328.  
 66 PR 16-MAY-1995; US-441871.  
 67 PA (GETH ) GENENTECH INC.  
 68 PI Matthews DJ, Wells JA, Zoller MJ:  
 69 WPI: 99-059058/05.  
 70 DR N-PSDB: V81689.  
 71 PI Selection of polypeptide substrates - using phagemid particles  
 72 displaying polypeptide(s) as coat protein fusions  
 73 Example 11; Fig 11; 8pp; English.  
 74 PS The present invention describes a method for selecting novel polypeptide  
 75 substrates. The method comprises: (a) constructing a replicable  
 76 expression vector comprising a transcription regulatory element operably  
 77 linked to a gene fusion; (b) mutating the vector at one or more selected  
 78 positions within the secretory-theta region to form a family of related  
 79 plasmids encoding substrate peptides; (c) transforming suitable host  
 80 cells with the plasmids; (d) infecting the transformed host cells with a  
 81 helper phage having a gene encoding the phage coat protein; (e) culturing  
 82 the transformed infected host cells under conditions suitable for forming  
 83 recombinant phagemid particles containing at least a portion of the  
 84 plasmid and capable of transforming the host; the conditions being  
 85 adjusted so that no more than a minor amount of phagemid particles  
 86 display more than one copy of the fusion protein on the surface of the  
 87 particles; (f) exposing the phagemid particles to a process capable of  
 88 modifying at least one covalent bond of an amino acid in the substrate  
 89 peptide of at least a portion of the phagemid particles; (g) contacting  
 90 the family of exposed phagemid particles with an affinity molecule, where

13 N-180, W-474.  
 14 New humanised antibody with affinity for vascular endothelial growth  
 15 factor (VEGF) for treatment of tumours, retinal disease and other  
 16 angiogenic states, also related nucleic acid, vectors and  
 17 transformed cells.  
 18 Example in Fig 8A-E: 100pp; English.  
 19 The present invention is directed to the Fab displaying antibody vector  
 20 (pMDL-1.1b), which is used in the course of the invention. The  
 21 specification describes humanised murine anti-vascular endothelial  
 22 growth factor (anti-VEGF) antibodies. The humanised antibodies  
 23 are used to inhibit VEGF induced angiogenesis, particularly for treating  
 24 or preventing tumours (of any type) and retinal disorders (e.g. age  
 25 related macular degeneration, diabetic retinopathy). They can also be  
 26 used to treat other conditions that involve angiogenesis, e.g. rheumatoid  
 27 arthritis, psoriasis, osteoarthritis, Grave's disease, etc.  
 28 Sequence: 237 AA:  
 29  
 30 Query Match: 86.1%; Score 1451; DB 1; Length 237;  
 31 Best local Similarity: 90.1%; Pred No 6.13e-169;  
 32 Matches: 219; Conservative: 9; Mismatches: 9; Indels: 5; Gaps: 4;  
 33  
 34 1 MKKNIAFLASMEVFSTAINAYADTQLTQSPSSLSASVGRVITTC-SA-S--QDIN-Y 55  
 35 1 MKKNIAFLASMEVFSTAINAYADTQLTQSPSSLSASVGRVITTCQSSSLVHGIGETY 60  
 36 56 LHWYKPKKAKPKKIIYSASELYSEVSPSPSSSSSGSDIFITLSSLPEDFAITYQDSI 115  
 37 61 LHWYKPKKAKPKKIIYSASELYSEVSPSPSSSSSGSDIFITLSSLPEDFAITYQDSI 120  
 38 116 TVWVDTGDTKVKETPAARSVFPPSPDEGLKSGTASVCLNNYFPRAKQWQVDN 175  
 39 121 HWVLTGGQTKVETPAARSVFPPSPDEGLKSGTASVCLNNYFPRAKQWQVDN 180  
 40 176 ALQSNSSQSVTFDESKTSTYSLSSITLTKADYKPKKVVVA-TVHUNLSSSVKPSNRG 235  
 41 181 ALQSNSSQSVTFDESKTSTYSLSSITLTKADYKPKKVVVA-TVHUNLSSSVKPSNRG 240  
 42 236 EC 237  
 43 241 EC 242  
 44  
 45 RESULT: 15  
 46 ID W83493 standard; Protein: 698 AA.  
 47 AC W83493;  
 48 DI 08-MAR-1999 (first entry)  
 49 DE 415 Fab molecule expressed on a phagemid surface.  
 50 KW Human: growth hormone; hGH; phagemid particle; enzyme substrate;  
 51 FN fusion gene; phage; protein coat.  
 52 OS Homo sapiens.  
 53 GS Synthetic.  
 54 PN US5846765-A.  
 55 PD 08-DEC-1998.  
 56 PF 16-MAY-1995; 441871.  
 57 PR 03-DEC-1993; US-161692.  
 58 PR 03-DEC-1990; US-621667.  
 59 PR 10-APR-1991; US-683400.  
 60 PR 14-JUN-1991; US-715300.  
 61 PR 09-AUG-1991; US-743614.  
 62 PR 03-DEC-1991; WO-009133.  
 63 PR 06-APR-1993; US-864452.  
 64 PR 30-APR-1993; US-050058.  
 65 PR 05-APR-1995; US-418328.  
 66 PR 16-MAY-1995; US-441871.  
 67 PA (GETH ) GENENTECH INC.  
 68 PI Matthews DJ, Wells JA, Zoller MJ:  
 69 WPI: 99-059058/05.  
 70 DR N-PSDB: V81689.  
 71 PI Selection of polypeptide substrates - using phagemid particles  
 72 displaying polypeptide(s) as coat protein fusions  
 73 Example 11; Fig 11; 8pp; English.  
 74 PS The present invention describes a method for selecting novel polypeptide  
 75 substrates. The method comprises: (a) constructing a replicable  
 76 expression vector comprising a transcription regulatory element operably  
 77 linked to a gene fusion; (b) mutating the vector at one or more selected  
 78 positions within the secretory-theta region to form a family of related  
 79 plasmids encoding substrate peptides; (c) transforming suitable host  
 80 cells with the plasmids; (d) infecting the transformed host cells with a  
 81 helper phage having a gene encoding the phage coat protein; (e) culturing  
 82 the transformed infected host cells under conditions suitable for forming  
 83 recombinant phagemid particles containing at least a portion of the  
 84 plasmid and capable of transforming the host; the conditions being  
 85 adjusted so that no more than a minor amount of phagemid particles  
 86 display more than one copy of the fusion protein on the surface of the  
 87 particles; (f) exposing the phagemid particles to a process capable of  
 88 modifying at least one covalent bond of an amino acid in the substrate  
 89 peptide of at least a portion of the phagemid particles; (g) contacting  
 90 the family of exposed phagemid particles with an affinity molecule, where

CC the affinity molecule has affinity for the amino acid residue having the  
CC modified covalent bond; and (h) separating the phagemid particles that  
CC bind to the affinity molecule from those that do not bind. The selection  
CC method is used for identifying enzyme substrates. The present sequence  
CC represents an 4D5 Fab molecule expressed on a phagemid surface from the  
CC present invention.  
SQ Sequence 598 AA;

Query Match 85 5%; Score 1437; DB 1; Length 698;  
Best Local Similarity 90.1%; Pred No 7.44e-99;  
Matches 219; Conservative 5; Mismatches 14; Indels 5; Gaps 3;  
Db 1 MKKNIAFLASVEFSIATNAYADIQMTQSPSSLSASVGGPVTITCPASQD-VN-TAVA- 57  
QY 1 MKKNIAFLASVEFSIATNAYADIQMTQSPSSLSASVGGPVTITCPASQD-VN-TAVA- 57  
Db 58 --WYDVKWPKAKLLIYASFLYSGVSPFSSPSSTGTFLLTSSLOPEDFATYYGQOHY 115  
QY 61 LHWYQKPFAPKLLIYKVSNEFSVPSPESSGSGTDTLLTSSLOPEDFATYYGQST 120  
Db 116 TTPPIFGQTKVEIKPTVAAPSVFIPTPPSDQIKSGTASVVCLNNFYPPFAKVMKVDN 175  
QY 121 HVPLTFGQTKVEIKPTVAAPSVFIPTPPSDQIKSGTASVVCLNNFYPPFAKVMKVDN 180  
Db 176 ALQSNQSESVTEQDSKSTYSLSSTILSKADYKHKVYACEVTHQGLSPVTKSFNRG 235  
QY 191 ALQSNQSESVTEQDSKSTYSLSSTILSKADYKHKVYACEVTHQGLSPVTKSFNRG 240  
Db 236 EC 237  
QY 241 EC 242

Search completed: Thu May 18 11:53:53 2000  
Job time : 19 secs.



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CC FILING DATE: 03-MAR-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Love, Richard B.
CC REGISTRATION NUMBER: 34,650
CC REFERENCE/DOCKET NUMBER: P0874P1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415/225-5530
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO.: 56:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 242 amino acids
CC TYPE: Amino Acid
CC TOPOLOGY: Linear
CC SEQUENCE 242 AA, 25430 MW, 332270 CN;

Query Match      89.9%; Score 1511; DB 1; Length 242;
Best Local Similarity 87.6%; Pred. No. 2,42e-98;
Matches 212; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

DB 1 MKKNIAFLASMFVSIATNAYADIVTQTPSLPSVLGDDQASISCPSSQSLSLVHGIGNTY 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QQ 1 MKKNIAFLASMFVSIATNAYADIVTQTPSLPSVLGDDQASISCPSSQSLSLVHGIGNTY 60
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DB 61 LHWLCKPGSQPKLLIYKVNPFSGVFDPFPFGSGSSTFTLPISPVPFAEDMGLYFCSQT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QQ 61 LHWLCKPGSQPKLLIYKVNPFSGVFDPFPFGSGSSTFTLPISPVPFAEDMGLYFCSQT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 HVPLTFQACTKELEKPAVAAPTVEIFPPSPSEQLKSGTASVVCLLNPNYPPEAKVQWVDN 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QQ 121 HVPLTFQACTKELEKPAVAAPTVEIFPPSPSEQLKSGTASVVCLLNPNYPPEAKVQWVDN 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 ALQSGNSQSVTEQDSKDYSLSTLTLSRADYEKKHVKVACEVTHOGLSSPVTKSFNRG 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QQ 181 ALQSGNSQSVTEQDSKDYSLSTLTLSRADYEKKHVKVACEVTHOGLSSPVTKSFNRG 240
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RESULT 3
ID US-08-398-613A-56 STANDARD: PPT: 242 AA.
XX AC xxxxxx
XX DT
XX DE
XX APPLICANT: Pong, Sherman
XX APPLICANT: Hebert, Caroline Alice
XX APPLICANT: Kim, Kyung Jin
XX TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory Disorders
XX NUMBER OF SEQUENCES: 58
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: Genentech, Inc.
XX STREET: 460 Point San Bruno Blvd
XX CITY: South San Francisco
XX STATE: California
XX COUNTRY: USA
XX ZIP: 94080
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: MicPatIn (Genentech)
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US-08/398-612A
XX FILING DATE: 01-MAR-1995
XX CLASSIFICATION: 424
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: 08/398611
XX FILING DATE: 01-MAR-1995
XX APPLICATION NUMBER: 08/398612
```



CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Genentech, Inc.  
 CC STREET: 460 Point San Bruno Blvd  
 CC CITY: South San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94080  
 CC  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: WinPatIn (Genentech)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/463.587A  
 CC FILING DATE: 05-Jun-1995  
 CC CLASSIFICATION: 435  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: 06/050058  
 CC FILING DATE: 30-APR-1993  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US91/09133  
 CC FILING DATE: 03-DEC-1991  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/743614  
 CC FILING DATE: 09-AUG-1991  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/715300  
 CC FILING DATE: 14-JUN-1991  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/683400  
 CC FILING DATE: 10-APR-1991  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/621667  
 CC FILING DATE: 03-DEC-1990  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Schwartz, Timothy P.  
 CC REGISTRATION NUMBER: 32171  
 CC REFERENCE/DOCKET NUMBER: P0645P4D2  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415/225-7467  
 CC TELEFAX: 415/952-9881  
 CC TELEX: 910/371-7168  
 CC INFORMATION FOR SEQ ID NO: 25:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 237 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC  
 CC SEQUENCE 237 AA; 25977 MW; 322792 CN;

Query Match 85.5%; Score 1437; DB 2; Length 237;  
 Best Local Similarity 90.1%; Pred No 5.62e-93;  
 Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;

Db 1 MKKNIAFLASMEVFSEIATNAYADIQMTQSPSSLSASVGDRTVITCRASQD-VN-TAVA- 57  
 QY 1 MKKNIAFLASMEVFSEIATNAYADIQMTQSPSSLSASVGDRTVITCRASQSLVHGIGETY 60  
 Db 58 --WYQOKPKGKAPKLLIYKVSVPFSGSGSGTDFTLTISLSQPEDFATYYCSQST 115  
 QY 61 LHWYQOKPKGKAPKLLIYKVSVPFSGSGSGTDFTLTISLSQPEDFATYYCSQST 120  
 Db 116 ITPTFGQGIKVEIKPTVAAPSVFIFPPSDEQIKGTASVVCCLNNFYPRKAKVQWVKVDN 175  
 QY 121 HVPLTEGGQGIKVEIKPTVAAPSVFIFPPSDEQIKGTASVVCCLNNFYPRKAKVQWVKVDN 180  
 Db 176 ALQSGNSQSVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 235  
 QY 191 ALQSGNSQSVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG 240  
 Db 236 EC 237  
 QY 241 EC 242

RESULT 6  
 ID PCT-US91-09133-26 STANDARD: PPT: 237 AA.  
 XX AC xxxxxx  
 XX DT  
 XX Sequence 26. Application PC/TUS9109133  
 XX DE  
 XX Sequence 26. Application PC/TUS9109133  
 CC GENERAL INFORMATION  
 CC APPLICANT: Genentech, Inc.  
 CC APPLICANT: Garrard, Lisa J.  
 CC APPLICANT: Hennen, Dennis J.  
 CC APPLICANT: Bass, Steven  
 CC APPLICANT: Greene, Ronald  
 CC APPLICANT: Lowman, Henry B.  
 CC APPLICANT: Wells, James A.  
 CC APPLICANT: Mathews, David J.  
 CC TITLE OF INVENTION: Enrichment Method For Variant Proteins  
 CC TITLE OF INVENTION: With Altered Binding Properties  
 CC NUMBER OF SEQUENCES: 27  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Genentech, Inc.  
 CC STREET: 460 Point San Bruno Blvd  
 CC CITY: South San Francisco  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94080  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: patin (Genentech)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US91/09133  
 CC FILING DATE: 19911203  
 CC CLASSIFICATION: 425  
 CC PRIOR APPLICATION DATA: 07/743614  
 CC APPLICATION NUMBER:  
 CC PRIOR APPLICATION DATA: 07/715300  
 CC APPLICATION NUMBER:  
 CC APPLICATION NUMBER: 07/683400  
 CC PRIOR APPLICATION DATA: 07/621667  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Benson, Robert H.  
 CC REGISTRATION NUMBER: 30,446  
 CC REFERENCE/DOCKET NUMBER: 645P4  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 415/266-1489  
 CC TELEFAX: 415/952-9881  
 CC TELEX: 910/371-7168  
 CC INFORMATION FOR SEQ ID NO: 26:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 237 amino acids  
 CC TYPE: AMINO ACID  
 CC TOPOLOGY: linear  
 CC SEQUENCE 237 AA; 25977 MW; 322792 CN;

Query Match 85.5%; Score 1437; DB 3; Length 237;  
 Best Local Similarity 90.1%; Pred No 5.62e-93;  
 Matches 218; Conservative 5; Mismatches 14; Indels 5; Gaps 3;

Db 1 MKKNIAFLASMEVFSEIATNAYADIQMTQSPSSLSASVGDRTVITCRASQD-VN-TAVA- 57  
 QY 1 MKKNIAFLASMEVFSEIATNAYADIQMTQSPSSLSASVGDRTVITCRASQSLVHGIGETY 60  
 Db 58 --WYQOKPKGKAPKLLIYKVSVPFSGSGSGTDFTLTISLSQPEDFATYYCSQST 115  
 QY 61 LHWYQOKPKGKAPKLLIYKVSVPFSGSGSGTDFTLTISLSQPEDFATYYCSQST 120





CC REFERENCE/DOCKET NUMBER: F1123  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 650/225-1489  
 CC TELEFAX: 650/952-9881  
 CC INFORMATION FOR SEQ ID NO: 17:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 218 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:

Query Match 80.3% Score 1350 DB 2: Length 218;  
 Best Local Similarity 90.9% Pred No 1: 134-86;  
 Matches 199; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

DL 1 DIQLTQSPSSLSASVGDPTITCPASKP-VQGEQSDSYLWVQKPKAPKLLIYAASYL 59  
 QY 24 DIQMTQSPSSLSASVGDPTITCPSSQSLVHIGETYLHWYQKPKAPKLLIYVVSNP 83  
 DB 60 SGVPSRFSGSSGDFTLTISSLPEDFATYYCQASHENPYTFGGSTKVEIKRTVAAPSV 119  
 QY 84 SGVPSRFSGSSGDFTLTISSLPEDFATYYCQASHENPYTFGGSTKVEIKRTVAAPSV 143  
 DB 120 FIFPPSDEQLKSTASVWVLLNNFYPPKAVKQVYVTHQGLSSPVTKSPNREG 218  
 QY 144 FIFPPSDEQLKSTASVWVLLNNFYPPKAVKQVYVTHQGLSSPVTKSPNREG 242  
 DE 180 FIFPPSDEQLKSTASVWVLLNNFYPPKAVKQVYVTHQGLSSPVTKSPNREG 218  
 QY 144 FIFPPSDEQLKSTASVWVLLNNFYPPKAVKQVYVTHQGLSSPVTKSPNREG 242

RESULT 9  
 ID US-09-987-352P-19 STANDARD: PPT: 218 AA  
 XX XXXXXX

Sequence 19 Application US/09887352P  
 Patent No. 5994511  
 GENERAL INFORMATION:  
 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
 TITLE OF INVENTION: Improving Polypeptides  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA: US/09/987/352P  
 APPLICATION NUMBER: 09/0887352P  
 FILING DATE: 03-Jul-1997  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET NUMBER: F1123  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:

CC LENGTH: 218 amino acids  
 CC TYPE: Amino Acid  
 CC TOPOLOGY: Linear  
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:

Query Match 80.3% Score 1350 DB 2: Length 218;  
 Best Local Similarity 90.9% Pred No 1: 134-86;  
 Matches 199; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

DB 1 DIQLTQSPSSLSASVGDPTITCPASKP-VQGEQSDSYLWVQKPKAPKLLIYAASYL 59  
 QY 24 DIQMTQSPSSLSASVGDPTITCPSSQSLVHIGETYLHWYQKPKAPKLLIYVVSNP 83  
 DB 60 SGVPSRFSGSSGDFTLTISSLPEDFATYYCQASHENPYTFGGSTKVEIKRTVAAPSV 119  
 QY 84 SGVPSRFSGSSGDFTLTISSLPEDFATYYCQASHENPYTFGGSTKVEIKRTVAAPSV 143  
 DB 120 FIFPPSDEQLKSTASVWVLLNNFYPPKAVKQVYVTHQGLSSPVTKSPNREG 218  
 QY 144 FIFPPSDEQLKSTASVWVLLNNFYPPKAVKQVYVTHQGLSSPVTKSPNREG 242  
 DB 180 FIFPPSDEQLKSTASVWVLLNNFYPPKAVKQVYVTHQGLSSPVTKSPNREG 218  
 QY 144 FIFPPSDEQLKSTASVWVLLNNFYPPKAVKQVYVTHQGLSSPVTKSPNREG 242

RESULT 10  
 ID US-09-987-352B-24 STANDARD: PPT: 218 AA  
 XX XXXXXX

Sequence 24 Application US/09887352B

Sequence 24, Application US/09887352B  
 Patent No. 5994511  
 GENERAL INFORMATION:  
 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
 TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
 TITLE OF INVENTION: Improving Polypeptides  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA: US/08/887/352B  
 APPLICATION NUMBER: US/08/887/352B  
 FILING DATE: 03-Jul-1997  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET NUMBER: F1123  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 218 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 CC SEQUENCE 218 AA: 23800 MW: 271009 CN:

Query Match 80.3% Score 1350 DB 2: Length 218;











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#authors      Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
              F.; Yamaki, S.; Kazi, H.; Takashi, I.; Shinoda, T.
#submission   submitted to JIPID, November 1998
#description   A new subgroup of kappa type light chains (Vkv) identified in
              cases of AL amyloidosis.
#accession    JE0243
#molecule_type protein
#residues     1-215 ##label ALI
SUMMARY       #length 215 #molecular-weight 23455 #checksum 9947

Query Match      72.8%; Score 1124; DB 2; Length 215;
Best Local Similarity 82.3%; Pred. No. 7.47e-173;
Matches 181; Conservative 18; Mismatches 15; Indels 6; Gaps 4;

Db 1 FVLTQSPATLSVSPGERATLISGASQSVHS--N--LAWYQCKPKQAPLLIYDASTRA 55
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLVHGIGETYLHWYQCKPKAPKLLIYKVSNEF 83
56 LQIPAFSSGSGIDFILLISLASEFALVYQYQNTWPLTFGGQTKVEIKRTVAAPS 115
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLVHGIGETYLHWYQCKPKAPKLLIYKVSNEF 83
84 SGVPSRFSGSGSGDFTLTISLSLQPEFAFYCSQTHVPLTFGGQTKVEIKRTVAAPS 142
116 VFIPFDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 175
QY 143 FIPFDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 202
176 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 215
QY 203 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 242

RESULT 3
ENTRY    JE0243 #type complete
TITLE    Ig kappa chain NIG93 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
05-Dec-1998

ACCESSIONS
REFERENCE JE0243
#authors  Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata,
              F.; Yamaki, S.; Kazi, H.; Takashi, I.; Shinoda, T.
#submission submitted to JIPID, November 1998
#description A new subgroup of kappa type light chains (Vkv) identified in
              cases of AL amyloidosis.
#accession JE0243
#molecule_type protein
#residues 1-215 ##label ALI
#length 215 #molecular-weight 23455 #checksum 9947

Query Match      70.3%; Score 1181; DB 2; Length 215;
Best Local Similarity 80.5%; Pred. No. 8.37e-166;
Matches 177; Conservative 17; Mismatches 20; Indels 6; Gaps 6;

Db 1 FVLTQSPATLSVSPGERATLISGASQSV--AT--NV--V--WYMKLGQAPLLIYDASTRA 55
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLVHGIGETYLHWYQCKPKAPKLLIYKVSNEF 83
56 LQIPAFSSGSGIDFILLISLASEFALVYQYQNTWPLTFGGQTKVEIKRTVAAPS 115
QY 84 SGVPSRFSGSGSGDFTLTISLSLQPEFAFYCSQTHVPLTFGGQTKVEIKRTVAAPS 142
116 VFIPFDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 175
QY 143 VFIPFDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 202
176 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 215
QY 203 LSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 242

RESULT 4
ENTRY    A23746 #type complete
TITLE    Ig kappa chain V-III (KAU cold agglutinin) - human

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ORGANISM #formal_name Homo sapiens #common_name man
DATE     30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change
16-Aug-1996

ACCESSIONS
REFERENCE A23746
#authors  Leonil, J.; Ghiso, J.; Goni, F.; Frangione, B.
              J. Biol. Chem. (1991) 266:2936-2942
#journal   The primary structure of the Fab fragment of protein KAU, a
              monoclonal immunoglobulin M cold agglutinin.
#cross-references MIMD:91131575
#accession A23746
#status    preliminary
#molecule_type protein
#residues 1-215 ##label LEO
KEYWORDS   heterotrimer; immunoglobulin
SUMMARY    #length 215 #molecular-weight 23050 #checksum 116

Query Match      67.8%; Score 1140; DB 2; Length 215;
Best Local Similarity 80.3%; Pred. No. 4.31e-159;
Matches 175; Conservative 16; Mismatches 23; Indels 4; Gaps 4;

Db 1 EIVLTQSPATLSVSPGERATLISGASQSV-S--SN--YLAWYQCKPKQAPLLIYDASTRA 56
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLVHGIGETYLHWYQCKPKAPKLLIYKVSNEF 83
57 TGIPDRFSGSGSDTDLTILSLRLEPEDFAVYQYQYGGSSPLIFGGGKVEIKRTVAAPS 116
QY 84 SGVPSRFSGSGSGDFTLTISLSLQPEFAFYCSQTHVPLTFGGQTKVEIKRTVAAPS 143
117 FIPFDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 176
QY 144 FIPFDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 203
177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 214
QY 204 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 241

RESULT 5
ENTRY    JE0241 #type complete
TITLE    Ig kappa chain AM37 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change
05-Dec-1998

ACCESSIONS
REFERENCE JE0241
#authors  Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima,
              M.; Takashi, I.; Shinoda, T.
#submission submitted to JIPID, November 1998
#description Structure relationship of kappa type light chains with AL
              amyloidosis: Multiple deletions found in a Vkv protein
#accession JE0241
#molecule_type protein
#residues 1-216 ##label ALI
SUMMARY    #length 216 #molecular-weight 23926 #checksum 4962

Query Match      67.3%; Score 1132; DB 2; Length 216;
Best Local Similarity 77.3%; Pred. No. 8.78e-158;
Matches 159; Conservative 15; Mismatches 32; Indels 3; Gaps 3;

Db 1 DIVLTQSPDPLAVSLGERATINCKSSQSVLYN--SKNFWYQCKPKQ--PKLLIW--ANYPE 57
QY 24 DIQMTQSPSSLSASVDGVITTCPSQSLVHGIGETYLHWYQCKPKAPKLLIYKVSNEF 83
58 SGVPSRFSGSGSGDFTLTILISLQAEVLVAVYQYQYVSTPSFGGGLKRTVAAPS 117
QY 84 SGVPSRFSGSGSGDFTLTILISLQPEFAFYCSQTHVPLTFGGQTKVEIKRTVAAPS 143
118 FIPFDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 177
QY 144 FIPFDEQLKSGTASVGLLNFFYPKAVQKVDNALQSGNSQESVTEQDSKSTYS 203
178 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNPGEC 216

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Matched protein - protein database search, using Smith-Waterman algorithm  
on: The May 18 11:45:24 2000. MaxStar time 78.78 seconds  
94554 Million cell updates/sec  
tabular output not generated.

Title: US-09-234-182A-62  
Description: (1.41) from US09234182A.ppt  
RefSeq Score: 1691  
Sequence: 1 MKEVHATLASMVFVETATH.....EVTHQGLSSPVTKSTNPGEC 242

Scoring Tables: PAM 160  
Gap 11  
Searched: 83877 seqs, 30454973 residues

Post processing: Minimum March 98  
Listing first 40 summaries  
Database: swissprot38  
1:swissprot

Statistics: Mean 45.768; Variance 74.944; scale 0.618  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
ID	Score	Query Match	Description		
1	721	42.9	IG KAPPA CHAIN V-III PE	1	54e-145
2	602	45.9	IG KAPPA CHAIN V-III PE	1	1.01e-115
3	575	44.2	IG KAPPA CHAIN V-III PE	5	15e-109
4	575	44.2	IG KAPPA CHAIN V-III PE	4	43e-106
5	566	44.0	IG KAPPA CHAIN V-III PE	6	54e-106
6	561	43.8	IG KAPPA CHAIN V-III PE	4	50e-104
7	561	43.8	IG KAPPA CHAIN V-III PE	2	54e-103
8	543	42.4	IG KAPPA CHAIN V-III PE	4	44e-103
9	543	42.4	IG KAPPA CHAIN V-III PE	2	47e-101
10	543	42.4	IG KAPPA CHAIN V-III PE	4	36e-100
11	547	42.5	IG KAPPA CHAIN V-III PE	4	36e-100
12	547	42.5	IG KAPPA CHAIN V-III PE	4	36e-100
13	544	42.4	IG KAPPA CHAIN V-III PE	7	59e-102
14	544	42.4	IG KAPPA CHAIN V-III PE	2	40e-101
15	544	42.4	IG KAPPA CHAIN V-III PE	2	40e-101
16	543	42.4	IG KAPPA CHAIN V-III PE	4	23e-101
17	542	42.3	IG KAPPA CHAIN V-III PE	7	47e-101
18	544	42.5	IG KAPPA CHAIN V-III PE	7	24e-100
19	547	42.5	IG KAPPA CHAIN V-III PE	1	28e-99
20	547	42.5	IG KAPPA CHAIN V-III PE	1	28e-99
21	547	42.5	IG KAPPA CHAIN V-III PE	1	28e-99
22	547	42.5	IG KAPPA CHAIN V-III PE	1	28e-99
23	544	42.4	IG KAPPA CHAIN V-III PE	3	97e-99
24	544	42.4	IG KAPPA CHAIN V-III PE	7	20e-99

24	530	31.5	113	1	KV2D_HUMAN	IG KAPPA CHAIN V-III PE	6.77e-98
25	530	31.5	114	1	KV4A_HUMAN	IG KAPPA CHAIN V-III PE	6.77e-98
26	526	31.3	108	1	KV1V_HUMAN	IG KAPPA CHAIN V-III PE	6.53e-97
27	526	31.3	108	1	KV1V_HUMAN	IG KAPPA CHAIN V-III PE	6.53e-97
28	526	31.3	108	1	KV1V_HUMAN	IG KAPPA CHAIN V-III PE	6.53e-97
29	526	31.3	108	1	KV1V_HUMAN	IG KAPPA CHAIN V-III PE	6.53e-97
30	520	30.9	117	1	KV2E_HUMAN	IG KAPPA CHAIN V-III PE	1.95e-95
31	517	30.8	112	1	KV3E_MOUSE	IG KAPPA CHAIN V-III PE	1.95e-95
32	517	30.8	112	1	KV3E_MOUSE	IG KAPPA CHAIN V-III PE	1.95e-95
33	514	30.6	109	1	KV3B_HUMAN	IG KAPPA CHAIN V-III PE	1.95e-95
34	514	30.6	109	1	KV3B_HUMAN	IG KAPPA CHAIN V-III PE	1.95e-95
35	514	30.6	112	1	KV3C_HUMAN	IG KAPPA CHAIN V-III PE	1.95e-95
36	514	30.6	112	1	KV3C_HUMAN	IG KAPPA CHAIN V-III PE	1.95e-95
37	513	30.5	113	1	KV3A_HUMAN	IG KAPPA CHAIN V-III PE	1.95e-95
38	512	30.5	108	1	KV1A_HUMAN	IG KAPPA CHAIN V-III PE	1.80e-93
39	512	30.5	108	1	KV3M_HUMAN	IG KAPPA CHAIN V-III PE	1.80e-93
40	510	30.3	108	1	KV3A_HUMAN	IG KAPPA CHAIN V-III PE	1.80e-93
41	509	30.3	109	1	KV3E_MOUSE	IG KAPPA CHAIN V-III PE	1.80e-93
42	509	30.3	111	1	KV3H_MOUSE	IG KAPPA CHAIN V-III PE	1.80e-93
43	508	30.2	109	1	KV3E_MOUSE	IG KAPPA CHAIN V-III PE	1.80e-93
44	507	30.2	109	1	KV3E_MOUSE	IG KAPPA CHAIN V-III PE	1.80e-93
45	506	30.1	109	1	KV3D_HUMAN	IG KAPPA CHAIN V-III PE	5.33e-92

ALIGNMENTS

RESULT 1 STANDARD: PRT: 106 AA.

AC KAC\_HUMAN  
AC P01834;  
DI 21-JUL-1996 (Rel. 01, Created)  
DI 21-JUL-1996 (Rel. 01, Last sequence update)  
DI 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN C REGION.  
GN IGKC.

OC Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE (MYELOMA PROTEIN EU).  
RX MEDLINE: 71064023.  
RA Gattilieri P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;  
FI "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
FI acid sequence of the light chain."  
RL Biochemistry 9:3155-3161(1970).  
RN [2]  
RP EU, DISULFIDE BONDS.  
RX MEDLINE: 71064027.  
RA Gall W.E., Edelman G.M.;  
FI "The covalent structure of a human gamma G-immunoglobulin. X.  
FI Intrachain disulfide bonds."  
RL Biochemistry 9:3188-3195(1970).  
RN [3]  
RP SEQUENCE (BENCE-JONES PROTEIN TI).  
RX MEDLINE: 72188439.  
RA Suter L., Barnikel H.U., Watanabe S., Hilschmann N.;  
FI "The antibody structure: the primary structure of a monoclonal  
FI immunoglobulin chain of kappa-type, subgroup 3 (Bence Jones protein  
FI ti). IV. The complete amino acid sequence and its significance for  
FI the mechanism of antibody production."  
RL Bence-Seyler's J. Physiol. Chem. 253:189-208(1972).  
RN [4]  
RP SEQUENCE (BENCE-JONES PROTEIN POY).  
RX MEDLINE: 81043304.  
RA Hietler P.A., Max E.E., Seidman J.G., Maizel J.V., Jr., Leder P.;  
FI "Cloned human and mouse kappa immunoglobulin constant and 3' region  
FI genes conserve homology in functional segments."  
RL Cell 23:197-207(1980).  
RN [5]  
RP SEQUENCE (BENCE-JONES PROTEIN POY).  
RX Hilschmann N., Barnikel H.U., Hess M., Langer R., Festschmal H.,  
RA Steinmetz-Kayne M., Suter L., Watanabe S.;  
FI (10) Franek F., Shugar D., eds.;  
FI gamma globulins: Structure and function, pp.37-74, Academic Press,

RC NEW YORK (1969).  
 RN [6]  
 RP SEQUENCE (BENCE-JONES PROTEIN CUM)  
 RX MEDLINE: 68242259.  
 RA Hilschmann N.F.  
 RT "The complete amino acid sequence of Bence Jones protein Gm (Kappa type)".  
 RL Biochem Biophys Res Commun 248:1718-1722(1997).  
 RN [7]  
 RP SEQUENCE (BENCE-JONES PROTEIN AG)  
 RX MEDLINE: 68234734.  
 RA Titani K., Shinoda T., Putnam F.W.  
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges".  
 RL J. Biol. Chem. 244:3550-3560(1969).  
 RN [8]  
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN CH)  
 RX MEDLINE: 70201507.  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.  
 RT "Macroglobulin structure. Variable sequence of light and heavy chains".  
 RL Science 169:56-59(1970).  
 CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER.  
 CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER. 45-ALA AND 83-LEU.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its context is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: J00241; AAA58989.1;  
 DR EMBL: V00557; CAA23923.1;  
 DR PIR: A02116; K3HU.  
 DR MIM: 147200;  
 DR PROSITE: PS00090; IG\_MHC; 1.  
 DR PFAM: PF00047; ig: 1.  
 KW Immunoglobulin domain; Immunoglobulin C region  
 FT NON\_TER 1  
 FT DISULFID 26 86  
 FT DISULFID 106 106  
 FT VARIANT 83 83  
 FT INTERCHAIN (WITH A HEAVY CHAIN).  
 FT V -> L (IN INV(1,2) MARKER).  
 FT /FTID=VAR\_003897.  
 FT D -> N (IN REF. 7 AND 8).  
 FT E -> Q (IN REF. 5 AND 6).  
 FT CONFLICT 14 14  
 FT CONFLICT 57 57  
 SEQUENCE 106 AA; 11609 MW; 51984D1FDD3722E8 CRC64;  
 Query Match 42.9%; Score 721; DB 1; Length 106.  
 Best Local Similarity 100.0%; Pred NO 1 54e-145;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DE 1 TVAAFSVLIFFSCDQLSGTAAVCLLNFPBEAVVMPVVALSGNSGNSVIFGFS 60  
 QY 137 TVAAFSVLIFFSCDQLSGTAAVCLLNFPBEAVVMPVVALSGNSGNSVIFGFS 196  
 DB 61 KDSVLSLSTILSKADYKHKVACEVTHGSLSPVTKSPNFGEC 106  
 QY 137 KDSVLSLSTILSKADYKHKVACEVTHGSLSPVTKSPNFGEC 242  
 RESULT 2  
 ID KY01.MOUSE STANDARD: FFT: 113 AA  
 AC P01631  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DI 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE IG KAPPA CHAIN V-II REGION 26-10  
 CS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Sutealia; Rodentia; Sciurognathi; Muridae; Murine; Mus.

PN SEQUENCE.  
 RP STRAIN-A/J;  
 RX MEDLINE: 83178921  
 RA Novotny J., Margolies M.N.  
 RT "Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody".  
 RL Biochemistry 22:1153-1159(1983).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA  
 CC PROTEIN THAT BINDS DIGOXIN.  
 DR PIR: A01914; KYMS26.  
 DR PFAM: PF00047; ig: 1  
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma  
 FT DOMAIN 1 23  
 FT DOMAIN 24 39  
 FT COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 40 54  
 FT FRAMEWORK 2.  
 FT DOMAIN 55 61  
 FT COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 62 93  
 FT FRAMEWORK 3.  
 FT DOMAIN 94 102  
 FT COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 103 112  
 FT FRAMEWORK 4.  
 FT DISULFID 23 93  
 FT NON\_TER 113 113  
 BY SIMILARITY.  
 SQ SEQUENCE 113 AA; 12273 MW; P0F99CE949AP4C2A CRC64;  
 Query Match 35.9%; Score 602; DB 1; Length 113;  
 Best Local Similarity 70.8%; Pred. NO. 1.01e-115;  
 Matches 80; Conservative 20; Mismatches 13; Indels 0; Gaps 0;  
 DB 1 DVMTQPLSLPVSLDQASISGRSSQSLVHSNGNYLWYLCFAQCSPTIIYVKSPPF 40  
 QY 24 DIQMTSPSLASVGDPTVITCPSSQSLVHGIGETVILHWYQCKPKAKPLLIYKVNPF 83  
 DB 61 SGVDPFRSSGSGTITLKISRVAEELGIYFSQTHVPTFGSGTKLEIRP 113  
 QY 84 SGVDPFRSSGSGTITLKISRVAEELGIYFSQTHVPTFGSGTKLEIRP 136  
 RESULT 3  
 ID KVLN.HUMAN STANDARD: FFT: 108 AA  
 AC P01606;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DI 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION OU.  
 CS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE: 70201507.  
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.  
 RT "Macroglobulin structure: variable sequence of light and heavy chains".  
 RL Science 169:56-59(1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.  
 DR PIR: A01872; KIHU01.  
 DR HSP: P01607; IPEI  
 DR PFAM: PF00047; ig: 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49  
 FT FRAMEWORK 2.  
 FT DOMAIN 50 56  
 FT COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88  
 FT FRAMEWORK 3.  
 FT DOMAIN 89 97  
 FT COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107  
 FT FRAMEWORK 4.  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 BY SIMILARITY.  
 SQ SEQUENCE 108 AA; 11777 MW; 82F3DA24A105827E CRC64;  
 Query Match 34.2%; Score 575; DB 1; Length 108;

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Waterman's protein database search, using Smith-Waterman algorithm  
on The May 18 11:47:09 2000: 53,086 Million cell updates/sec  
Label: output not reported.  
Time: 05:29:24 100A 62  
Percent Score: 100.00 from 0.00 to 100.00  
Sequence: 1 MREHAFGLAFVMSVSIIN.....EVHGLSFFVTSFNSGEC 242

Protein Label: FAM 150  
Tag 11  
Searched: 22579 seqs, 6144122 residues  
Post processing: Minimum Match 0  
Clustering: First 45 summaries  
On Index: split 12  
1: sp\_archaea 2: sp\_bacteria 3: sp\_fungi 4: sp\_human  
5: sp\_invertebrate 6: sp\_mammal 7: sp\_rh 8: sp\_rodent  
9: sp\_rh 10: sp\_plant 11: sp\_rodent 12: sp\_unclassified  
13: sp\_viruses 14: sp\_virus

Statistics: Mean 44.125, Variance 77.597, score 0.568  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES			
Protein	No.	Score	Match
1	1	1.00	1.00
2	1	1.00	1.00
3	1	1.00	1.00
4	1	1.00	1.00
5	1	1.00	1.00
6	1	1.00	1.00
7	1	1.00	1.00
8	1	1.00	1.00
9	1	1.00	1.00
10	1	1.00	1.00
11	1	1.00	1.00
12	1	1.00	1.00
13	1	1.00	1.00
14	1	1.00	1.00
15	1	1.00	1.00
16	1	1.00	1.00
17	1	1.00	1.00
18	1	1.00	1.00
19	1	1.00	1.00
20	1	1.00	1.00
21	1	1.00	1.00
22	1	1.00	1.00
23	1	1.00	1.00
24	1	1.00	1.00
25	1	1.00	1.00
26	1	1.00	1.00
27	1	1.00	1.00
28	1	1.00	1.00
29	1	1.00	1.00
30	1	1.00	1.00
31	1	1.00	1.00
32	1	1.00	1.00
33	1	1.00	1.00
34	1	1.00	1.00
35	1	1.00	1.00
36	1	1.00	1.00
37	1	1.00	1.00
38	1	1.00	1.00
39	1	1.00	1.00
40	1	1.00	1.00
41	1	1.00	1.00
42	1	1.00	1.00
43	1	1.00	1.00
44	1	1.00	1.00
45	1	1.00	1.00

RESULT	1	PRELIMINARY	PRT: 509 AA.
ID	008907		
AC	008907		
DI	01-JUL-1997 (Trembl, 04, Created)		
DT	01-JUL-1997 (Trembl, 04, Last sequence update)		
ET	01-NOV-1999 (Trembl, 12, Last annotation update)		
DE	BRAIN IMMUNOLOGICAL-LIKE PROTEIN (BIT)		
GN	BIT		
OS	Mus musculus (Mouse)		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
PC	SPIRIN-BALRYC, TISSUE-BRAIN:		
FX	MEDLINE: 97230468.		
FA	OHNISHI H., KUBOTA M., SANO S.		
FT	"BIT (Bit) maps to mouse chromosome 2."		
PL	Genomics 40:504-506(1997).		
DR	EMBL: D85785; BAA20376.1		
DR	MGI: 107947; Bit.		
DR	PFAM: PF00047; Ig: 3.		
SE	SEQUENCE 509 AA: 56033 MW: 40220008 CD0321		

ALIGNMENTS

Query Match	Score	DB 11	Length	Q99:
Best Local Similarity	25.84	1378	25	
Matches	52	Conserved	52	Matches 52
12	12	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
13	13	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
14	14	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
15	15	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
16	16	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
17	17	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
18	18	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
19	19	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
20	20	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
21	21	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
22	22	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
23	23	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
24	24	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
25	25	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
26	26	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
27	27	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
28	28	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
29	29	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
30	30	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
31	31	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
32	32	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
33	33	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
34	34	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
35	35	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
36	36	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
37	37	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
38	38	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
39	39	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
40	40	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
41	41	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
42	42	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
43	43	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
44	44	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		
45	45	LLASAPTSPTAIDTEVAVTIFENSVVAASGSLIRNIVISGLI-K3-PIRMYR-71		

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RESULT 2
ID Q0440 PRELIMINARY: PFI: 397 AA.
AC Q0440
DI 01-NOV-1999 (TrEMBLrel. 12, Created)
DI 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DI 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE D5576H24.2 (SHP-2) (SIGNAL REGULATOR PROTEIN BETA 1)
GN D5576H24.2
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthalia; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MATTHEWS L.
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL049634; CAB4661.1;
SQ SEQUENCE 397 AA: 43033 MW: 9091505 GPC32;
Query Match 13.5%; Score 227; DB 4; Length 397;
Best Local Similarity 26.6%; Pred No 2 250-24;
Matches 61; Conservative 63; Mismatches 98; Indels 21; Gaps 20;
DL 13 FELLITLLTGVAGDELVQVPEKSVSAAGESATLPGAMTSLIP-VQPI-M-WEP 68
QY 5 AFLASVFVSIAINAYADIMTSPSSLSASVGEVITICPSSLSLVH31SETVLRWY 65
DB 69 G-AG-APPELLYNGEHPPTVVELTKPNKLDPSISNITPADAGTYCVKPKFGS 126
QY 66 KFKAKKLLIYKVN-RFSGVPSFSGSGGT-IFTLTISSIQEDPATYCSQ-STHP 122
DL 127 KCVVEVSEATLSEVPKFSAPV-VSGGAVPATFHTVSPFCESHGSPPTIKWPN 185
QY 123 P-LTPGQGTVEIK-PTVAAPSVFTTPSDQKSGTASVCLLNPNYPPKAKVQW-KV 178
DL 195 UNED-3-DEFTNV-DRAGESVSSISHTAPVWLPCTVSC-V-ICEAHITL 233
QY 179 DNALQSNQSVSVIEKSDISLSL-SSI-LILSKALAEKHKVACEVTHQL 225
RESULT 3
ID F8324 PRELIMINARY: PFI: 503 AA.
AC F8324
DI 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-NOV-1998 (TrEMBLrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR
(SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SHPS-1) (SIGNAL-
REGULATOR PROTEIN ALPHA-1) (STEP-ALPHA1) (MID-1 ANTIGEN)
GN PIPNEL OF SHPS-1 OF D5576H24.1
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthalia; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-BRAIN:
RX MEDLINE: 97222999.
RA YAMAO T., HALLAKI T., AMANO K., MATSUDA Y., IAPAKASHI N., ICHI E.,
RA FUKIYA Y., KASUGA M.
PT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
localization of genes."
PL Biochem. Biophys. Res. Commun. 231:61-67(1997)
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=PLACENTA:
RA KUARIKONKOV A., CHEN Z., SUPES I., WANG H., SCHILLING J.,
RA GURICH A.
PT "A family of proteins that inhibit signalling through tyrosine kinase
receptors."
RL Nature 386:181-186(1997)
RN [3]
RP SEQUENCE OF 145-503 FROM N.A.
RA BATES K.

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PL Submitted (MAP-1999) to the EMBL/GenBank/DBJ databases.
DI FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE PHOSPHATASE
2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS
CC MITOGENS AND CELL ADHESION. MAY ACT AS A DOCKING PROTEIN AND
CC INDUCE TRANSLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA
CC MEMBRANE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN BRAIN.
CC HIGH LEVELS ALSO PRESENT IN HEART, SPLEEN, TESTIS, OVARY AND
CC PERIPHERAL BLOOD LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY CONTAINS
CC TWO C1-LIKE AND ONE V-LIKE DOMAINS.
DR EMBL: D86043; RAA12974.1;
DR EMBL: Y10375; CAA71403.1;
DR EMBL: AL034562; CAB38874.1;
DR MIM: 602461;
DR PFAM: PF00047; Iq: 3
KW Signal: Transmembrane; Alternative splicing; Immunoglobulin domain;
KW Glycoprotein; SH2-binding; Phosphorylation.
FT SIGNAL 1 26
FT CHAIN 27 503
FT DOMAIN 27 372
FT TRANSMEM 373 393
FT DOMAIN 394 503
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 129
FT IG-LIKE C1-TYPE DOMAIN.
FT DOMAIN 164 233
FT DOMAIN 266 339
FT SH2-BINDING (POTENTIAL).
FT DOMAIN 428 431
FT SH2-BINDING (POTENTIAL).
FT DOMAIN 438 443
FT SH3-BINDING (POTENTIAL).
FT DOMAIN 452 455
FT SH2-BINDING (POTENTIAL).
FT DOMAIN 459 472
FT SH2-BINDING (POTENTIAL).
FT DOMAIN 495 498
FT MOD_RES 428 428
FT MOD_RES 452 452
FT MOD_RES 460 469
FT MOD_RES 495 495
FT CARBOHYD 244 244
FT CARBOHYD 269 269
FT CARBOHYD 291 291
FT CARBOHYD 318 318
FT CARBOHYD 319 319
SQ SEQUENCE 503 AA: 54912 MW: 90A5272F GPC32;
Query Match 13.5%; Score 227; DB 4; Length 503;
Best Local Similarity 26.6%; Pred No 2 250-24;
Matches 61; Conservative 57; Mismatches 94; Indels 17; Gaps 17;
DL 17 LLAASSTANSVAGE-EMQVITQKSVSAAGESAHLGTVT-SLIP-VQ-P-ICWFG 71
QY 7 FLASVFVSIAINAYADIMTSPSSLSASVGEVITICPSSLSLVH31GTYLHWYQQ 66
DB 72 -AG-FAPELLYNGEHPPTVVELTKPNKLDPSISNITPADAGTYCVKPKFGSP 129
QY 67 KFKAKKLLIYKVN-RFSGVPSFSGSGGT-IFTLTISSIQEDPATYCSQ-STHP 123
DB 130 DTEKSGAATLSPKPSAPV-VSGPAARATPQHTVSPFCESHGSPPTIKWFKNGN 188
QY 124 LT-PGQGTVEIK-PTVAAPSVFTTPSDQKSGTASVCLLNPNYPPKAKVQW-KVDN 180
DB 189 EL-S-DFQTNV-DPVGESVSYSHIAKVLTRDVHSQVCEVAHVTL 234
QY 181 ALQSNQSVSVIEKSDISLSLSTLTSKADYKHKVACEVTHQL 229
RESULT 4
ID Q0241 PRELIMINARY: PFI: 398 AA.
AC Q0241
DI 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-AUG-1999 (TrEMBLrel. 11, Last annotation update)
DE SIGNAL-REGULATOR PROTEIN BETA-1 PRECURSOR (SHP-BETA1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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